

TABLE 2

BIOLOGICAL ACTIVITY OF SCI MUTANTS

	5	Mutant No.	Residue No.	Mutation	Size on Native Gel	AUC [mean]	Structure	Receptor Binding	% WT
		0		LD78	WT	160	Wt	1	100
10	1	48		Gln>Glu	Large?	400	Wt	2	
	2	44		Lys>Glu	Small	16	D	4	5
		45		Arg>Gln					
	5	17		Arg>Ser	Mixed	57.5	T/Do	2	25
15	10	26		Asp>Ala	Small	35	T	1	77.4
	11	12		Phe>Gln	Mixed	98	T/Do	1	34
	26	28		Phe>Glu	Small	16	D	4	1
		47		Arg>Glu					
20	28	29		Glu>Arg	Small		T	2	7.7
	29	18		Gln>Glu	Small	130	Do	1	
	30	17		Arg>Ser	Small	41	T	3	4.2
		18		Gln>Glu					
25	35	-3		>Leu	WT	155	Wt	4	3
		-2		>Ser					
		-1		>Ala					
	1			Ser>Pro					
30	38			Gly>Ser					
	46			Ser>Gly					
	37	5		Asp>Ser	WT		Wt	1	45
	38	24		Ile>Ala	WT		Wt	1	50
35	40	29		Glu>Ser	WT			4	
	42	44		Lys>Ser	Small	45	T/Do	1	18
	43	45		Arg>Ser	Small	25	T	3	
	45	52		Asp>Ser	WT			4	
40	48	60		Lys>Ser	WT			1	
	52	66		Glu>Ser	Large	27	T	1	161.5
	54	1		Ser>Ala	WT			1	145
	60	8		Thr>Ala	WT			1	
45	62	13		Ser>Ala	Large	370	Wt	1	66
	63	16		Ser>Ala	WT			3	
	64	18		Gln>Ser	Large	200	Wt	4	
	66	27		Tyr>Ala	WT			2	47
50	68	35		Ser>Ala	WT		Wt	1	125
	70	48		Gln>Ser	Mixed			2	

TABLE 2 (cont'd)

Mutant No.	Residue No.	Mutation	Size on Native Gel	AUC [mean]	Structure	Receptor Binding	% WT
5	71	53	Pro>Ala	WT		3	
	75	67	Leu>Ala	WT		1	
	77	12	Phe>Ala	Small	150	3	
	79	15	Thr>Ala	Small	180	1	
10	82	22	Asn>Ser	WT		1	
	84	25	Ala>Ser	WT		1	
	85	28	Phe>Ala	WT		3	
	87	31	Ser>Ala	WT		3	
15	94	42	Leu>Ala	WT		1	
	97	51	Ala>Ser	Mixed		2	
	101	26	Asp>Ala	WT		2	
		29	Glu>Arg				
20	102	26	Asp>Ala	Small		4	
		29	Glu>Arg				
		47	Arg>Glu				

KEY : AUC = Analytical Ultra Centrifugation (kDa)

Receptor Binding: 1 = Wild-type
 2 = 1/10 to 1/2 Wt
 3 = 1/100-1/10 Wt
 4 = Inactive

T = Tetramer

T/Do = Tetramer/Dodecamer equilibrium

D = Dimer

WT = Wild type

30

The following facts emerge from this analysis:

1)The majority of the variants with wild-type or minimally affected multimerisation properties exhibit wild-type or close to wild-type receptor binding.

35

2)There is a clear subset of variants which, though wild-type with respect to size, are clearly affected in their ability to compete with wild-type LD78 for receptor binding. The mutations in these variants presumably define the residues involved in interacting with the receptor. These key residues include Lys-44, Arg-45, Arg-17, Gln-18, Phe-28 and Glu-29.

40

3)Most of the de-multimerised variants appear to be compromised in receptor binding. This implies either that the residues involved in multimerisation are also involved in receptor binding, or that receptor binding requires a multimeric form of LD78. Wild-type receptor binding activity has not been seen in variants smaller than a tetramer. This is summarised in Figure 19. The numerals refer to the number of mutants found in each category. Mutants shown lying between the tetramer and dodecamer positions represent an equilibrium between the two states.

5
10 4)Variants in which the N terminus of LD78 are extended show greatly diminished ability to compete for receptor binding. Surprisingly, these include the forms of LD78 described previously such as in variant #35 (WO-A-9104274) and variant #34 (JP-A-03228683). In contrast, deletion of N-terminal residues appears to have minimal effect on receptor binding. The other N-terminal form described in the literature (Pragnell *et al.*, CRC Beatson Laboratories Scientific Report, Beatson Institute for Cancer Research, Glasgow, Scotland) does not express in the yeast expression systems described in this application.

15
20 5)The residues implicated in receptor binding map to two defined regions on the surface of the LD78 model described above. One region flanks the N-terminal serine and includes residues in the β -turn around residues 44-48 (Lys-Arg-Ser-Arg-Gln).

25 Taken together, these data suggest that the active form of LD78 is a tetramer. Figure 20 shows a view of the model of tetrameric LD78, showing the dramatic clustering of residues implicated in receptor binding. In this model of LD78 structure and function, mutations at the interface between dimers exert their effect on receptor binding indirectly, by disrupting the formation of the active, tetrameric species. A second implication of this model is that the N-terminal extended forms of LD78 are probably inactive proforms of the molecule, at least as regards the receptor present on A4 cells.

Both of these conclusions are surprising in view of the prior art. In WO-A-9104274 the N-termini of the LD78 forms they describe was not defined. The material was apparently biologically active, perhaps as a result of processing by proteases present in their *in vitro* assay of colony formation, or in view of the high concentrations of material used.

Although the active species of the SCI family of molecules has been a matter for speculation, it was recently asserted that for LD78 the active species is a monomer (Mantel *et al.*, (1992), *loc. cit.*). This was based on the observation that *E.coli*-derived LD78, disaggregated in 30% acetonitrile & 0.1% TFA, was 1000-fold more active in various *in vitro* colony forming unit assays on the haematosis lineage precursors BFU-E and GM-CFC cells. We can only speculate that this large difference reflects a problem with the activity of the aggregated *E.coli* derived material.

Example 165 - Demultimerised mutants can inhibit the proliferation of haemopoietic progenitor cells (Day 12 CFU-S)

The ability of mutant #10 (Example 7) to inhibit the formation of murine day 12 CFU-S cell colonies was measured *in vitro* according to the following method. The activity was compared to that of mutant #82 (Example 94), which is wild-type with respect to structure and receptor binding.

Day 12 CFU-S cells were sorted from normal murine bone marrow cells as described in Lord and Spooncer (1986) *Lymphokine Research* 5:59-72. Sorted cells (between 500-1000) were plated in soft agar and assayed for their colony forming ability according to the method described in Heyworth and Spooncer (1992) in "Haemopoiesis - A Practical Approach" page 37 IRL Press (Testa and Molineux, Eds).

Growth factors were supplied from conditioned medium of L cells and AF1-19T cells. Each of the conditioned media was used at 10% as described in Pragnell *et al.*, (1988) *Blood* 72:196-201. LD78 mutant 10 or 82 was added at 150ng/ml, 15ng/ml, 1.5ng/ml or 0.15ng/ml to the top agar in 10 μ l of PBS and allowed to diffuse through teh plate. The plates were then incubated at 37°C in 5% O₂, 5% CO₂ for 14 days. Colonies were counted with an inverted microscope. All assays were run in triplicate. 150ng/ml of LD78 wild type protein of Preparations 1 to 4 and PBS were used as controls in this experiment.

- 10 Results were expressed as a percentage of the control treted with carrier PBS alone. The Mutant 10 used in this assay will inhibit colony formation fo day 12 CFU-S cells at concentrations down to 1.5ng/ml. Both mutant 10 (Figure 24) and 82 (Figure 25) show similar potency with optimum inhibitors at 15ng/ml. This shows that a demultimerised variant can exert functional effects as well as binding
15 to the receptor.

Appendix A

Media recipes

5 BMGC

Quantities per litre:

	Sodium phosphate buffer 1M, pH6	- 100mL
10	Casamino acids (100g/L)	- 100mL
	Yeast Nitrogen Base (13.4 g/L)	- 100mL
	Biotin (0.2g/L)	- 2mL
	Glycerol	- 10mL

15 Filter sterilise

BMMC

As above but replace glycerol with 5mL of methanol.

20

YEPD

	Yeast extract	10g/L
	Peptone	20g/L
25	Glucose	10g/L

For solid medium add 15g/L agar

Autoclave at 121°C 15mins

YEPGlycerol

As above but replace glucose with glycerol

5 HCD

	H_3PO_4 (85%)	21mL/L
	$\text{CaSO}_4 \cdot \text{H}_2\text{O}$	0.9 g/L
	K_2SO_4	14.28g/L
10	$\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$	11.7g/L
	KOH	3.9g/L
	Glycerol	50g/L

15 pH is about 1.7 when made up. Bring pH to 4 in the fermentor with ammonia solution (prior to sterilization). Sterilize in the fermentor and bring pH to 5.85 with ammonia solution prior to inoculation.

To the 3.5L of medium in the fermentor add 10mL of the following trace element solution (PTM₁)

20

	$\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$	6g/L
	KI	0.8g/L
	$\text{MnSO}_4 \cdot \text{H}_2\text{O}$	3.0g/L
	$\text{NaMoO}_4 \cdot 2\text{H}_2\text{O}$	0.2g/L
25	H_3BO_3	0.02g/L
	$\text{CoCl}_2 \cdot 6\text{H}_2\text{O}$	0.5g/L
	ZnSO_4	20g/L
	H_2SO_4	5mL/L
	$\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$	65g/L
30	Biotin	0.2g/L

MD

	Yeast nitrogen base	13.4g/L
	Biotin	0.4g/L
5	Glucose	20g/L

Filter sterilise

For solid medium add 15g/L agar

10

Transformation buffers and reagentsSED

15	Sorbitol	1M
	EDTA (pH8)	25mM
	DTT	50mM (add just prior to use)

SCE

20

Sorbitol	1M
EDTA	1mM
Sodium citrate buffer pH5.8	10mM

25 CAS

Sorbitol	1M
Tris-Cl pH7.5	10mM
CaCl ₂	10mM

PEG solution

	PEG 3350	200g/L
	Tris-Cl pH7.5	10mM
5	CaCl ₂	10mM

Prepare fresh and filter sterilise. Discard if pH is below 7.

SOS

10	Sorbitol	1M
	YEPD	x0.3
	CaCl ₂	10mM

15 Regeneration medium (RD)

	Sorbitol	186g/L
	Agarose	10g/L
	Glucose	20g/L
20	Yeast nitrogen base	1.34g/L
	Biotin	400ug/L
	Histidine assay medium *	2g/L
	Glutamic acid	50mg/L
	Methionine	50mg/L
25	Lysine	50mg/L
	Leucine	50mg/L
	Isoleucine	50mg/L

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30 For base plates use agarose at 20g/L

ADDITIONAL REFERENCES

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Wingfield *et al*, *Eur.J.Biochem.*, 173, 65-72, (1988).

Patent number AU-B-63882/86

Wolpe and Cerami, *FASEB, J.* 3 2565-2573 (1989)

Yphantis, *Biochemistry*, 3, 297-317, (1964)

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5

(i) APPLICANT:

- (A) NAME: British Bio-technology Limited (non US)
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15 (B) STREET: British Bio-technology Limited, Watlington Road
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(E) COUNTRY: GB
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(B) STREET: British Bio-technology Limited, Watlington Road
(C) CITY: Cowley, Oxford
5 (E) COUNTRY: GB
(F) POSTAL CODE (ZIP): OX4 5LY

(ii) TITLE OF INVENTION: Stem Cell Inhibiting Proteins

10 (iii) NUMBER OF SEQUENCES: 178

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
15 (B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
(EPO)

(vi) PRIOR APPLICATION DATA:

- 20 (A) APPLICATION NUMBER: GB 9127319.3
(B) FILING DATE: 23-DEC-1991

(vii) PRIOR APPLICATION DATA:

- 25 (A) APPLICATION NUMBER: GB 9221587.0
(B) FILING DATE: 14-OCT-1992

(2) INFORMATION FOR SEQ ID NO:1:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

(iii) ANTI-SENSE: NO

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(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..229
- (D) OTHER INFORMATION: /codon_start= 1
/product= "LD78 SYNTHETIC GENE"

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(ix) FEATURE:

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- (A) NAME/KEY: 3'UTR
- (B) LOCATION: 223..225
- (D) OTHER INFORMATION: /function= "NON-TRANSLATED STOP CODON"

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- (A) NAME/KEY: 3'UTR
- (B) LOCATION: 226..228
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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Ser Leu Asp Lys Arg Ser Leu Ala Ala Asp Thr Pro Thr Ala Cys Cys

25

1

5

10

15

TTC TCT TAC ACC TCT AGA CAA ATT CCA CAA AAT TTC ATT GCT GAC TAC
96

Phe Ser Tyr Thr Ser Arg Gln Ile Pro Gln Asn Phe Ile Ala Asp Tyr

30

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35

TTT GAA ACT TCT TCT CAA TGT TCC AAG CCA GGT GTC ATC TTC TTG ACT
144

Phe Glu Thr Ser Ser Gln Cys Ser Lys Pro Gly Val Ile Phe Leu Thr

40

35

40

45

AAG CGC TCG AGA CAA GTC TGT GCT GAC CCA TCT GAA GAA TGG GTT CAA
 192
 5 Lys Arg Ser Arg Gln Val Cys Ala Asp Pro Ser Glu Glu Trp Val Gln
 50 55 60

10 AAA TAT GTT TCT GAC TTG GAA TTG TCT GCC TAA TAA G
 229
 Lys Tyr Val Ser Asp Leu Glu Leu Ser Ala * *
 65 70 75

15 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 76 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ser Leu Asp Lys Arg Ser Leu Ala Ala Asp Thr Pro Thr Ala Cys Cys
 1 5 10 15

30 Phe Ser Tyr Thr Ser Arg Gln Ile Pro Gln Asn Phe Ile Ala Asp Tyr
 20 25 30

35 Phe Glu Thr Ser Ser Gln Cys Ser Lys Pro Gly Val Ile Phe Leu Thr
 35 40 45

40 Lys Arg Ser Arg Gln Val Cys Ala Asp Pro Ser Glu Glu Trp Val Gln
 50 55 60

Lys Tyr Val Ser Asp Leu Glu Leu Ser Ala * *
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5 (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

15 (iii) ANTI-SENSE: YES

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 25 120
 AAGAAAGTTTC AAAGTAGTCA GCAATGAAAT TTTGTGGAAT TTGTCTAGAG GTGTAAGAGA
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 30 AACAAACAAGC GGTTGGAGTG TCAGCAGCCA AGGATCTTT ATCCAAGCT
 229

(2) INFORMATION FOR SEQ ID NO:4:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
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- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

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- (A) NAME/KEY: misc_feature
(B) LOCATION: 1..45
(D) OTHER INFORMATION: /product= "OLIGOMER FOR
CONSTRUCTION OF SYNTHETIC LD78 GENE"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA

5 (ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1..48
(D) OTHER INFORMATION: /product= "OLIGOMER FOR
CONSTRUCTION OF SYNTHETIC LD78 GENE"

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGAAACAAACA AGCGGTTGGA GTGTCAGCAG CCAAGGATCT TTTATCCA

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35 (2) INFORMATION FOR SEQ ID NO:6:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA

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- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..50
- (D) OTHER INFORMATION: /product= "OLIGOMER FOR CONSTRUCTION OF SYNTHETIC LD78 GENE"

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(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA

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- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..50
- (D) OTHER INFORMATION: /product= "OLIGOMER FOR CONSTRUCTION OF SYNTHETIC LD78 GENE"

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(2) INFORMATION FOR SEQ ID NO:8:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA

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(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..48
- (D) OTHER INFORMATION: /product= "OLIGOMER FOR CONSTRUCTION OF LD78 SYNTHETIC GENE"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

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48

(2) INFORMATION FOR SEQ ID NO:9:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

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- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..48

(D) OTHER INFORMATION: /product= "OLIGOMER FOR
CONSTRUCTION OF SYNTHETIC LD78 GENE"

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCGCTTAGTC AAGAAGATGA CACCTGGCTT GGAACATTGA GAAGAACT
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- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- 15 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

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(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..46
- (D) OTHER INFORMATION: /product= "OLIGOMER FOR THE
25 CONSTRUCTION OF LD78 SYNTHETIC GENE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

30 TAAGCGCTCG AGACAAGTCT GTGCTGACCC ATCTGAAGAA TGGGTT
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(2) INFORMATION FOR SEQ ID NO:11:

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- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

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- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..46
- (D) OTHER INFORMATION: /product= "OLIGOMER FOR CONSTRUCTION OF SYNTHETIC LD78 GENE"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATTTTGAAAC CCATTCTTCA GATGGGTCAAG CACAGACTTG TCTCGA
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(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

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- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..40
- (D) OTHER INFORMATION: /product= "OLIGOMER FOR CONSTRUCTION OF SYNTHETIC LD78 GENE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

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CAAAAAATATG TTTCTGACTT GGAATTGTCT GCCTAATAAG
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(2) INFORMATION FOR SEQ ID NO:13:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA

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(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1..37
(D) OTHER INFORMATION: /product= "OLIGOMER FOR
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GTTCCTCCAG TCANCGAC

18

(2) INFORMATION FOR SEQ ID NO:15:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7859 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 5 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TTCCCATGTC TCTACTGGTG GTGGTGCTTC TTTGGAATTA TTGGAAGGTA AGGAATTGCC
60

15

AGGTGTTGCT TTCTTATCCG AAAAGAAATA AATTGAATTG AATTGAATC GATAGATCAA
120

20

TTTTTTTCTT TTCTCTTCC CCATCCTTTA CGCTAAAATA ATAGTTTATT TTATTTTTG
180

AATATTTTTT ATTTATATAC GTATATATAG ACTATTATTT ACTTTTAATA GATTATTAAG
240

25

ATTTTTATTA AAAAAAAATT CGTCCCTCTT TTTAATGCCT TTTATGCAGT TTTTTTTCC
300

CATTCGATAT TTCTATGTC GGGTTTCAGC GTATTTAAG TTTAATAACT CGAAAATTCT
360

30

GCGTTTCGAA AAAGCTCTGC ATTAATGAAT CGGCCAACGC GCGGGGAGAG GCGGTTTGCG
420

35

TATTGGGCGC TCTTCCGCTT CCTCGCTCAC TGACTCGCTG CGCTCGGTG TTGGCTGCG
480

GCGAGCGGTA TCAGCTCACT CAAAGGCGGT AATACGGTTA TCCACAGAAT CAGGGGATAA
540

40

CGCAGGAAAG AACATGTGAG CAAAAGGCCA GCAAAAGGCC AGGAACCGTA AAAAGGCCGC

600
GTTGCTGGCG TTTTCCATA GGCTCCGCC CCCTGACGAG CATCACAAAA ATCGACGCTC
660
5 AAGTCAGAGG TGGCGAAACC CGACAGGACT ATAAAGATAC CAGGCGTTTC CCCCTGGAAG
720
CTCCCTCGTG CGCTCTCCTG TTCCGACCCCT GCCGCTTACC GGATACCTGT CCGCCTTCT
10 780
CCCTCGGGA AGCGTGGCGC TTTCTCATAG CTCACGCTGT AGGTATCTCA GTTCGGTGT
840
15 GGTCGTTCGC TCCAAGCTGG GCTGTGTGCA CGAACCCCCC GTTCAGCCCG ACCGCTGC
900
CTTATCCGGT AACTATCGTC TTGAGTCAA CCCGGTAAGA CACGACTTAT CGCCACTGGC
960
20 AGCAGCCACT GGTAACAGGA TTAGCAGAGC GAGGTATGTA GGCGGTGCTA CAGAGTTCTT
1020
GAAGTGGTGG CCTAACTACG GCTACACTAG AAGGACAGTA TTTGGTATCT GCGCTCTGCT
25 1080
GAAGCCAGTT ACCTTCGGAA AAAGAGTTGG TAGCTTTGA TCCGGCAAAC AAACCACCGC
1140
30 TGGTAGCGGT GGTTTTTG TTTGCAAGCA GCAGATTACG CGCAGAAAAA AAGGATCTCA
1200
AGAAGATCCT TTGATCTTT CTACGGGTC TGACGCTCAG TGGAACGAAA ACTCACGTTA
1260
35 AGGGATTTG GTCATGAGAT TATCAAAAAG GATCTTCACC TAGATCCTTT TAAATAAAAA
1320
ATGAAGTTT AAATCAATCT AAAGTATATA TGAGTAAACT TGGTCTGACA GTTACCAATG
40 1380

CTTAATCAGT GAGGCACCTA TCTCAGCGAT CTGTCTATT CGTCATCCA TAGTTGCCTG
 1440

ACTCCCCGTC GTGTAGATAA CTACGATAACG GGAGGGCTTA CCATCTGGCC CCAGTGCTGC
 5 1500

AATGATACCG CGAGACCCAC GCTCACCGGC TCCAGATTAA TCAGCAATAA ACCAGCCAGC
 1560

10 CGGAAGGGCC GAGCGCAGAA GTGGTCCTGC AACTTTATCC GCCTCCATCC AGTCTATTAA
 1620

TTGTTGCCGG GAAGCTAGAG TAAGTAGTTC GCCAGTTAAT AGTTTGCAGA ACAGTTGTTGC
 1680

15 CATTGCTACA GGCATCGTGG TGTACGCTC GTCGTTGGT ATGGCTTCAT TCAGCTCCGG
 1740

20 TTCCCAACGA TCAAGGCGAG TTACATGATC CCCCATGTTG TGCAAAAAAG CGGTTAGCTC
 1800

CTTCGGTCTT CCGATCGTTG TCAGAAGTAA GTTGGCCGCA GTGTTATCAC TCATGGTTAT
 1860

25 GGCAGCACTG CATAATTCTC TTACTGTCAT GCCATCCGTA AGATGCTTT CTGTGACTGG
 1920

TGAGTACTCA ACCAAGTCAT TCTGAGAATA GTGTATGCGG CGACCGAGTT GCTCTGCC
 1980

30 GGC GTCAACA CGGGATAATA CCGCGCCACA TAGCAGAACT TTAAAAGTGC TCATCATTGG
 2040

AAAACGTTCT TCGGGGCGAA AACTCTCAAG GATCTTACCG CTGTTGAGAT CCAGTTCGAT
 35 2100

GTAACCCACT CGTGCACCCA ACTGATCTTC AGCATCTTT ACTTTCACCA GCGTTCTGG
 2160

40 GTGAGCAAAA ACAGGAAGGC AAAATGCCGC AAAAAAGGGA ATAAGGGCGA CACGGAAATG

2220

TTGAATACTC ATACTCTTCC TTTTCATAA TTATTGAAGC ATTTATCAGG GTTATTGTCT
2280

5 CATGAGCGGA TACATATTG AATGTATTAA GAAAAATAAA CAAATAGGGG TTCCGCGCAC
2340

ATTTCCCCGA AAAGTGCCAC CTGACGTCTA AGAAACCATT ATTATCATGA CATTAACCTA
10 2400

TAAAAATAGG CGTATCACGA GGCCCTTCG TCTTCAGAA TTCTGAACCA GTCCTAAAAC
2460

15 GAGTAATAG GACCGGCAAT TCTTCAGCA ATAAACAGGA ATACCAATTA TTAAAAGATA
2520

ACTTAGTCAG ATCGTACAAT AAAGCTAGCT TTGAAGAAAA ATGCGCCTTA TTCAATCTT
20 2580

GCTATAAAAAA ATGGCCAAA ATCTCACATT GGAAGACATT TGATGACCTC ATTTCTTCA
2640

ATGAAGGGCC TAACGGAGTT GACTAATGTT GTGGAAATT GGAGCGATAA GCGTGCTTCT
25 2700

GCCGTGGCCA GGACAACGTA TACTCATCAG ATAACAGCAA TACCTGATCA CTACTTCGCA
2760

30 CTAGTTCTC GGTACTATGC ATATGATCCA ATATCAAAGG AAATGATAGC ATTGAAGGAT
2820

GAGACTAATC CAATTGAGGA GTGGCAGCAT ATAGAACAGC TAAAGGGTAG TGCTGAAGGA
2880

35 AGCATAACGAT ACCCCGCATG GAATGGATA ATATCACAGG AGGTACTAGA CTACCTTCA
2940

TCCTACATAA ATAGACGCAT ATAAGTACGC ATTTAAGCAT AACACACGCAC TATGCCGTTC
40 3000

TTCTCATGTA TATATATATA CAGGCAACAC GCAGATATAG GTGCGACGTG AACAGTGAGC
 3060

5 TGTATGTGCG CAGCTCGCGT TGCATTTCG GAAGCCCTCG TTTTCGGAAA CGCTTTGAAG
 3120

10 TTCCTATTCC GAAGTTCCTA TTCTCTAGAA ACTATAGGAA CTTCAGAGCG CTTTGAAAAA
 3180

15 CCAAAAGCGC TCTGAAGACG CACTTCAAA AAACCAAAAA CGCACCGGAC TGTAACGAGC
 3240

20 TACTAAAATA TTGCGAATAC CGCTTCCACA AACATTGCTC AAAAGTATCT CTTTGCTATA
 3300

25 TATCTCTGTG CTATATCCCT ATATAACCTA CCCATCCACC TTTCGCTCCT TGAACTTGCA
 3360

30 TCTAAACTCG ACCTCTACAT TTTTATGTT TATCTCTAGT ATTACTCTT AGACAAAAAA
 3420

35 ATTGTAGTAA GAACTATTCA TAGAGTGAAT CGAAAACAAT ACGAAAATGT AAACATTCC
 3480

40 TATACGTAGT ATATAGAGAC AAAATAGAAG AAACCGTTCA TAATTTCTG ACCAATGAAG
 3540

45 AATCATCAAC GCTATCACTT TCTGTTACA AAGTATGCGC AATCCACATC GGTATAGAAT
 3600

50 ATAATCGGGG ATGCCTTAT CTTGAAAAAA TGCACCCGCA GCTTCGCTAG TAATCAGTAA
 3660

55 ACGCAGGAAG TGGAGTCAGG CTTTTTTAT GGAAGAGAAA ATAGACACCA AAGTAGCCTT
 3720

60 CTTCTAACCT TAACGGACCT ACAGTGCAA AAGTTATCAA GAGACTGCAT TATAGAGCGC
 3780

65 ACAAAGGAGA AAAAAAGTAA TCTAAGATGC TTTGTTAGAA AAATAGCGCT CTCGGGATGC

3840
ATTTTGTAG AACAAAAAAG AAGTATAGAT TCTTTGTTGG TAAAATAGCG CTCTCGCGTT
3900

5
GCATTTCTGT TCTGTAAAAA TGCAAGCTCAG ATTCTTGTT TGAAAAATTAA GCGCTCTCGC
3960

GTTGCATTT TGTTTACAA AAATGAAGCA CAGATTCTTC GTTGGTAAAA TAGCGCTTTC
10 4020

GCGTTGCATT TCTGTTCTGT AAAAATGCAG CTCAGATTCT TTGTTTGAAA AATTAGCGCT
4080

15 CTCGCCTTGC ATTTTGTTC TACAAAATGA AGCACAGATG CTTCGTTAAC AAAGATATGC
4140

TATTGAAGTG CAAGATGGAA ACCGAGAAAA TGAACCGGGG ATGCGACGTG CAAGATTACC
4200

20 TATGCAATAG ATGCAATAGT TTCTCCAGGA ACCGAAATAC ATACATTGTC TTCCGTAAAG
4260

CGCTAGACTA TATATTATTA TACAGGTTCA AATATACTAT CTGTTTCAGG GAAACTCCC
25 4320

AGGTTCGGAT GTTCAAAATT CAATGATGGG TAACAAGTAC GATCGTAAAT CTGTAAAACA
4380

30 GTTTGTCGGA TATTAGGCTG TATCTCCTCA AAGCGTATTC GAATATCATT GAGAAGCTGC
4440

ATTTTTTTT TTTTTTATAT ATATTCAG GATATACCAT TGTAATGCCT GCCCCTAAGA
4500

35 AGATCGTCGT TTTGCCAGGT GACCACGTTG GTCAAGAAAT CACAGCCGAA GCCATTAAGG
4560

TTCTTAAAGC TATTTCTGAT GTTCGTTCCA ATGTCAAGTT CGATTTCGAA AATCATTAA
40 4620

TTGGTGGTGC TGCTATCGAT GCTACAGGTG TTCCACTTCC AGATGAGGCG CTGGAAGCCT
 4680

CCAAGAAGGC TGATGCCGTT TTGTTAGGTG CTGTGGTGG TCCTAAATGG GGTACCGGTA
 5 4740

GTGTTAGACC TGAACAAGGT TTACTAAAAA TCCGTAAAGA ACTTCAATTG TACGCCAACT
 4800

10 TAAGACCATG TAACTTGCA TCCGACTCTC TTTTAGACTT ATCTCCAATC AAGCCACAAAT
 4860

TTGCTAAAGG TACTGACTTC GTTGTGTTA GAGAATTAGT GGGAGGTATT TACTTGGTA
 4920

15 AGAGAAAGGA AGACGATGGT GATGGTGTG CTTGGGATAG TGAACAAATAC ACCGTTCCAG
 4980

AAGTCAAAG AATCACAAAGA ATGGCCGCTT TCATGCCCT ACAACATGAG CCACCATTGC
 20 5040

CTATGGTC CTTGGATAAA GCTAATGTTT TGGCCTCTTC AAGATTATGG AGAAAAACTG
 5100

25 TGGAGGAAAC CATCAAGAAC GAATTCCCTA CATTGAAAGT TCAACATCAA TTGATTGATT
 5160

CTGCCGCCAT GATCCTAGTT AAGAACCCAA CCCACCTAAA TGGTATTATA ATCACCAAGCA
 5220

30 ACATGTTGG TGATATCATC TCCGATGAAG CCTCCGTTAT CCCAGGCTCC TTGGGTTTGT
 5280

TGCCATCTGC GTCCTGGCC TCTTGCCAG ACAAGAACAC CGCATTGGT TTGTACGAAC
 35 5340

CATGCCATGG TTCCGCTCCA GATTGCCAA AGAATAAGGT CAACCCTATC GCCACTATCT
 5400

40 TGTCTGCTGC AATGATGTTG AAATTGTCAT TGAACCTGCC TGAAGAAGGT AAAGCCATTG

5460

AAGATGCAGT TAAAAAGGTT TTGGATGCAG GTATCAGAAC TGGTGATTAA GGTGGTTCCA
5520

5 ACAGTACCAAC CGAAGTCGGT GATGCTGTGG CCGAAGAAAGT TAAGAAAATC CTTGCTTAAA
5580

AAGATTCTCT TTTTTATGA TATTTGTACA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
10 5640

AAAAAAAAAA AAAAAAAAAA AAAATGCAGC GTCACATCGG ATAATAATGA TGGCAGCCAT
5700

15 TGTAGAAGTG CCTTTGCAT TTCTAGTCTC TTTCTCGGTC TAGCTAGTT TACTACATCG
5760

CGAAGATAGA ATCTTAGATC ACAC TGCTGAGCTG GATCAATAGA GTAACAAAAG
5820

20 AGTGGTAAGG CCTCGTTAAA GGACAAGGAC CTGAGCGGAA GTGTATCGTA CAGTAGACGG
5880

AGTATACTAG TATAGTCTAT AGTCCGTGGA ATTCTCATGT TTGACAGCTT ATCATCGATA
25 5940

AGCTAGCTTT CTAACTGATC TATCCAAAAC TGAAAATTAC ATTCTTGATT AGGTTTATCA
6000

30 CAGGCAAATG TAATTTGTGG TATTTGCCG TTCAAAATCT GTAGAATTTC CTCATTGGTC
6060

ACATTACAAC CTGAAAATAC TTTATCTACA ATCATACCAT TCTTAATAAC ATGTCCCCTT
6120

35 AATACTAGGA TCAGGCATGA ACGCATCACA GACAAAATCT TCTTGACAAA CGTCACAATT
6180

GATCCCTCCC CATCCGTAT CACAATGACA GGTGTCATTT TGTGCTTTA TGGGACGATC
40 6240

CTTATTACCG CTTTCATCCG GTGATTGACC GCCACAGAGG GGCAGAGAGC AATCATCAC
 6300

TGCAAACCT TCTATACACT CACATCTACC AGTGATCGAA TTGCATTCAAG AAAACTGTTT
 5 6360

GCATTCAAAA ATAGGTAGCA TACAATTAAA ACATGGCGGG CATGTATCAT TGCCCTTATC
 6420

10 TTGTGCAGTT AGACGCGAAT TTTTCAAGA AGTACCTTCA AAGAATGGGG TCTTATCTTG
 6480

TTTTCAAGT ACCACTGAGC AGGATAATAA TAGAAATGAT AATATACTAT AGTAGAGATA
 6540

15 ACGTCGATGA CTTCCCATAAC TGTAATTGCT TTTAGTTGTG TATTTTTAGT GTGCAAGTTT
 6600

CTGTAAATCG ATTAATTTTT TTTTCTTCC TCTTTTATT AACCTTAATT TTTATTTAG
 20 6660

ATTCCCTGACT TCAACTCAAG ACCCACAGAT ATTATAACAT CTGCATAATA GGCATTTGCA
 6720

25 AGAATTACTC GTGAGTAAGG AAAGAGTGAG GAACTATCGC ATACCTGCAT TTAAAGATGC
 6780

CGATTTGGGC GCGAACCTT TATTTGGCT TCACCCCTCAT ACTATTATCA GGGCCAGAAA
 6840

30 AAGGAAGTGT TTCCCTCCTT CTTGAATTGA TGTTACCCCTC ATAAAGCACG TGGCCTCTTA
 6900

TCGAGAAAGA AATTACCGTC GCTCGTGATT TGTTGCAAA AAGAACAAAA CTGAAAAAAC
 35 6960

CCAGACACGC TCGACTTCCT GTCTTCCTAT TGATTGCAGC TTCCAATTTC GTCACACAAAC
 7020

40 AAGGTCTAG CGACGGCTCA CAGGTTTGT AACAAAGCAAT CGAAGGTTCT GGAATGGCGG

7080

GGAAAGGGTT TAGTACCAACA TGCTATGATG CCCACTGTGA TCTCCAGAGC AAAGTCGTT
7140

5 CGATCGTACT GTACTCTCTC TCTTCAAAC AGAATTGTCC GAATCGTGTG ACAACAAACAG
7200

CCTGTTCTCA CACACTCTT TCTTCTAACCC AAGGGGGTGG TTTAGTTTAG TAGAACCTCG
10 7260

TGAAACTTAC ATTTACATAT ATATAAACTT GCATAAATTG GTCAATGGAA GAAATACATA
7320

15 TTTGGTCTTT TCTAATTGCT AGTTTTCAA GTTCTTAGAT GCTTTCTTT TCTCTTTTT
7380

ACAGATCATC AAGGAAGTAA TTATCTACTT TTTACAACAA ATACAAAAGA TCTATGAGAT
7440

20 TTCCTTCAAT TTTTACTGCA GTTTTATTG CAGCATCCTC CGCATTAGCT GCTCCAGTCA
7500

ACACTACAAC AGAAGATGAA ACGGCACAAA TTCCGGCTGA AGCTGTCATC GGTTACTTAG
25 7560

ATTTAGAAGG GGATTTCGAT GTTGCTGTT TGCCATTTTC CAACAGCACA AATAACGGGT
7620

30 TATTGTTAT AAATACTACT ATTGCCAGCA TTGCTGCTAA AGAAGAAGGG GTAAGCTTGG
7680

ATAAAAGAAA CAGCGACTCT GAATGCCCGC TGAGCCATGA TGGCTACTGC CTGCACGACG
7740

35 GTGTATGCAT GTATATCGAA GCTCTGGACA AATACGCATG CAACTGCGTA GTTGGTTACA
7800

TCGGCGAACG TTGCCAGTAC CGCGACCTGA AATGGTGGGA GCTCCGTTAA TAAGGATCC
40 7859

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

15 AGGATGGGAA AAGAGAA

17

(2) INFORMATION FOR SEQ ID NO:17:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: DNA (genomic)

(iii) ANTI-SENSE: NO

30

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..234
- (D) OTHER INFORMATION: /codon_start= 1
/product= "MIP-1-ALPHA GENE"

35

(ix) FEATURE:

- (A) NAME/KEY: 3'UTR
- (B) LOCATION: 223..225
- (D) OTHER INFORMATION: /function= "UNTRANSLATED STOP

40

CODON™

(ix) FEATURE:

(A) NAME/KEY: 3'UTR

5 (B) LOCATION: 226..228

(D) OTHER INFORMATION: /function= "NON-TRANSLATED STOP CODON"

CODON™

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGC TTA CCT GCC ATG GCG CCT TAT GGA GCT GAC ACC CCG ACT GCA TGC
48

Ser Leu Pro Ala Met Ala Pro Tyr Gly Ala Asp Thr Pro Thr Ala Cys

15

1

5

10

15

TGC TTC TCC TAC AGC CGG AAG ATT CCA CGC CAA TTC ATC GTC GAC TAT
96

Cys Phe Ser Tyr Ser Arg Lys Ile Pro Arg Gln Phe Ile Val Asp Tyr

25

TTT GAA ACT AGT AGC CTT TGC TCC CAG CCA GGT GTC ATT TTC CTG ACT

144

Phe Glu Thr Ser Ser Leu Cys Ser Gln Pro Gly Val Ile Phe Leu Thr

30

35

40

45

AAG AGA AAC CGG CAG ATC TGC GCT GAC TCC AAA GAG ACC TGG GTC CAA
192

35 Lys Arg Asp Arg Gln Ile Cys Ala Asp Ser Lys Glu Thr Trp Val Gln

50

55

60

GAA TAG ATC ACT GAC CTC GAG CTG AAT GCC TGA TAG GAT CCG

234

Glu Tyr Ile Thr Asp Leu Glu Leu Asn Ala * * Asp Pro
 65 70 75

5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- 10 (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Ser Leu Pro Ala Met Ala Pro Tyr Gly Ala Asp Thr Pro Thr Ala Cys
 1 5 10 15

20

Cys Phe Ser Tyr Ser Arg Lys Ile Pro Arg Gln Phe Ile Val Asp Tyr
 20 25 30

25

Phe Glu Thr Ser Ser Leu Cys Ser Gln Pro Gly Val Ile Phe Leu Thr
 35 40 45

30

Lys Arg Asn Arg Gln Ile Cys Ala Asp Ser Lys Glu Thr Trp Val Gln
 50 55 60

35

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- 40 (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

5

(iii) ANTI-SENSE: YES

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CGGATCCTAT CAGGCATTCA GCTCGAGGTC AGTGATGTAT TCTTGGACCC AGGTCTCTTT
60

15 GGAGTCAGCG CAGATCTGCC GGTTTCTCTT AGTCAGGAAA ATGACACCTG GCTGGGAGCA
120

AAGGCTACTA GTTTCAAAAT AGTCGACGAT GAATTGGCGT GGAATCTTCC GGCTGTAGGA
180

20 GAAGCAGCAT GCAGTCGGGG TGTCAAGCTCC ATAAGGCGCC ATGGCAGGTA AGCT
234

(2) INFORMATION FOR SEQ ID NO:20:

25

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA

35

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1..38
(D) OTHER INFORMATION: /product= "OLIGOMER FOR
CONSTRUCTION OF MIP-ALPHA GENE"

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AGCTTACCTG CCATGGCGCC TTATGGAGCT GACACCCC

38

5

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- 10 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

15

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..41
- 20 (D) OTHER INFORMATION: /product= "OLIGOMER FOR CONSTRUCITON OF MIP1-ALPHA GENE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

25

TGCAGTCGGG GTGTCAGCTC CATAAGGCAG CATGGCAGGT A

41

(2) INFORMATION FOR SEQ ID NO:22:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- 35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

40

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1..44
(D) OTHER INFORMATION: /product= "OLIGOMER FOR
CONSTRUCTION OF MIP1-ALPHA GENE"

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

10 GACTGCATGC TGCTTCTCCT ACAGCCGGAA GATTCCACGC CAAT
44

(2) INFORMATION FOR SEQ ID NO:23:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ACGATGAATT GGC GTGGAAT CTTCCGGCTG TAGGAGAAGC AGCA
44

35 (2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

5

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..39
- (D) OTHER INFORMATION: /product= "OLIGOMER FOR CONSTRUCTION OF MIP1-ALPHA GENE"

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

15 TCATCGTCGA CTATTTGAA ACTAGTAGCC TTTGCTCCC

39

(2) INFORMATION FOR SEQ ID NO:25:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

30

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..39
- (D) OTHER INFORMATION: /product= "OLIGOMER FOR CONSTRUCTION OF MIP1-ALPHA GENE"

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCTGGCTGGG AGCAAAGGCT ACTAGTTCA AATAGTCG

39

40

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

10

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..37
- (D) OTHER INFORMATION: /product= "OLIGOMER FOR CONSTRUCTION OF MIP1-ALPHA GENE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

20

AGCCAGGTGT CATTTCCTG ACTAAGAGAA ACCGGCA

37

(2) INFORMATION FOR SEQ ID NO:27:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA

35

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..37
- (D) OTHER INFORMATION: /product= "OLIGOMER FOR CONSTRUCTION OF MIP1-ALPHA GENE"

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GCAGATCTGC CGGTTCTCT TAGTCAGGAA AATGACA

37

5

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

15

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..44
- (D) OTHER INFORMATION: /product= "OLIGOMER FOR THE CONSTRUCTION OF MIP1-ALPHA GENE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

25

GATCTGCGCT GACTCCAAAG AGACCTGGGT CCAAGAATAC ATCA

44

30

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: DNA

40

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1..44
(D) OTHER INFORMATION: /product= "OLIGOMER FOR
CONSTRUCTION OF MIP1-ALPHA GENE"

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AGGTCAGTGA TGTATTCTTG GACCCAGGTC TCTTTGGAGT CAGC
10 44

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
15 (A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

25 (A) NAME/KEY: misc_feature
(B) LOCATION: 1..32
(D) OTHER INFORMATION: /product= "OLIGOMER FOR
CONSTRUCTION OF MIP1-ALPHA SYNTHETIC GENE"

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CTGACCTCGA GCTGAATGCC TGATAGGATC CG
32

35 (2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

5

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..29
- (D) OTHER INFORMATION: /product= "OLIGOMER FOR CONSTRUCTION OF MIP1-ALPHA GENE"

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

15 AATTCCGGATC CTATCAGGCA TTCAGCTCG

29

(2) INFORMATION FOR SEQ ID NO:32:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: DNA

30

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..15
- (D) OTHER INFORMATION: /product= "TOP STRAND OF OLIGONUCLEOTIDE ADAPTOR"

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

AGCTTGGATA AAAGA

15

40

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

10

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..11
- (D) OTHER INFORMATION: /product= "BOTTOM STRAND OF OLIGONUCLEOTIDE ADAPTOR"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

20

TCTTTTATCC A

11

(2) INFORMATION FOR SEQ ID NO:34:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA (genomic)

(iii) ANTI-SENSE: NO

35

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..228
- (D) OTHER INFORMATION: /codon_start= 1

40

/product= "HUMAN ACT-2 SYNTHETIC GENE"

(ix) FEATURE:

(A) NAME/KEY: 3'UTR

5 (B) LOCATION: 223..225

(D) OTHER INFORMATION: /function= "NON-TRANSLATED STOP
CODON"

(ix) FEATURE:

10 (A) NAME/KEY: 3'UTR

(B) LOCATION: 226..228

(D) OTHER INFORMATION: /function= "NON-TRANSLATED STOP
CODON"

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AGC TTG GAT AAA AGA GCA CCA ATG GGT TCA GAC CCT CCA ACC GCA TGC
48

20 Ser Leu Asp Lys Arg Ala Pro Met Gly Ser Asp Pro Pro Thr Ala Cys

1

5

10

15

25 TGC TTT TCT TAC ACC GCT AGG AAG TTG CCT AGA AAC TTT GTG GTC GAC
96

Cys Phe Ser Tyr Thr Ala Arg Lys Leu Pro Arg Asn Phe Val Val Asp

20

25

30

30

TAC TAT GAG ACC TCT TCT TTG TGC TCC CAG CCA GCT GTG GTA TTC CAA
144

Tyr Tyr Glu Thr Ser Ser Leu Cys Ser Gln Pro Ala Val Val Phe Gln

35

35

40

45

40 ACC AAA AGA TCC AAG CAA GTC TGT GCT GAC CCG AGT GAA TCC TGG GTC
192

Thr Lys Arg Ser Lys Gln Val Cys Ala Asp Pro Ser Glu Ser Trp Val

50

55

60

5

CAG GAG TAC GTG TAT GAC TTG GAA TTG AAC TGA TAAG

229

Gln Glu Tyr Val Tyr Asp Leu Glu Leu Asn *

65

70

75

10

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Ser Leu Asp Lys Arg Ala Pro Met Gly Ser Asp Pro Pro Thr Ala Cys
1 5 10 15

25

Cys Phe Ser Tyr Thr Ala Arg Lys Leu Pro Arg Asn Phe Val Val Asp
20 25 30

30

Tyr Tyr Glu Thr Ser Ser Leu Cys Ser Gln Pro Ala Val Val Phe Gln
35 40 45

35

Thr Lys Arg Ser Lys Gln Val Cys Ala Asp Pro Ser Glu Ser Trp Val
50 55 60

40

Gln Glu Tyr Val Tyr Asp Leu Glu Leu Asn *

65

70

75

*

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 229 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA (genomic)

(iii) ANTI-SENSE: YES

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CTTATCAGTT CAATTCCAAG TCATAACACGT ACTCCTGGAC CCAGGATTCA CTGGGGTCAG

60

20

CACAGACTTG CTTGGATCTT TTGGTTTGGAA ATACCACAGC TGGCTGGGAG CACAAAGAAG

120

25

AGGTCTCATA GTAGTCGACC ACAAAAGTTTC TAGGCCACTT CCTAGCGGTG TAAAGAAAAGC

180

AGCATGCGGT TGGAGGGTCT GAACCCATTG GTGCTCTTTT ATCCAAGCT

229

30

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

40

5

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..46
- (D) OTHER INFORMATION: /product= "OLIGOMER FOR CONSTRUCTION OF HUMAN ACT-2 GENE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

10 AGCTTGGATA AAAGAGCACC AATGGGTTCA GACCCCTCAA CCGCAT

46

(2) INFORMATION FOR SEQ ID NO:38:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

25

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..45
- (D) OTHER INFORMATION: /product= "OLIGOMER FOR CONSTRUCTION OF HUMAN ACT-2 GENE"

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AGCATGCGGT TGGAGGGTCT GAACCCATTG GTGCTCTTT ATCCA

45

35

(2) INFORMATION FOR SEQ ID NO:39:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

5

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..47
- (D) OTHER INFORMATION: /product= "Oligomer for construction of human ACT-2 gene"

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

15

GCTGCTTTTC TTACACCGCT AGGAAGTTGC CTAGAAACTT TGTGGTC

47

(2) INFORMATION FOR SEQ ID NO:40:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: DNA

30

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..51
- (D) OTHER INFORMATION: /product= "Oligomer for construction of human ACT-2 gene"

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

AGTAGTCGAC CACAAAGTTT CTAGGCAACT TCCTAGCGGT GTAAGAAAAG C

40

51

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

10

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..46
- (D) OTHER INFORMATION: /product= "Oligomer for construction of human ACT-2 gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

20

GACTACTATG AGACCTCTTC TTTGTGCTCC CAGCCAGCTG TGGTAT

46

(2) INFORMATION FOR SEQ ID NO:42:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA

35

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..46
- (D) OTHER INFORMATION: /product= "Oligomer for construction of human ACT-2 gene"

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GTTTGGATA CCACAGCTGG CTGGGAGCAC AAAGAAGAGG TCTCAT

46

5

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

15

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..47
- (D) OTHER INFORMATION: /product= "Oligomer for construction of human ACT-2 gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

25

TCCAAACCAA AAGATCCAAG CAAGTCTGTG CTGACCCGAG TGAATCC

47

(2) INFORMATION FOR SEQ ID NO:44:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

40

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1..47
(D) OTHER INFORMATION: /product= "Oligomer for construction of human ACT-2 gene"

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GGACCCAGGA TTCACTCGGG TCAGCACAGA CTTGCTTGGA TCTTTTG

10

47

(2) INFORMATION FOR SEQ ID NO:45:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

25

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..43
- (D) OTHER INFORMATION: /pr
construction of hum

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TGGGTCCAGG AGTACGTGTA TGACTTGGAA TTGAACGTAT AAG

43

35

(2) INFORMATION FOR SEO ID NO: 46:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

5

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..40
- (D) OTHER INFORMATION: /product= "Oligomer for
construction of human ACT-2 gene"

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

15 GATCCTTATC AGTTCAATTG CAAGTCATAAC ACGTACTCCT

40

(2) INFORMATION FOR SEQ ID NO:47:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GTTTTCCCAG TCACGAC

17

35

(2) INFORMATION FOR SEQ ID NO:48:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GCACAGACTT CTCTCGAGCG CT

10 22

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- 25 (A) NAME/KEY: misc_feature
(B) LOCATION: 1..30
(D) OTHER INFORMATION: /product= "BB6299 oligomer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

30 GACTTGTCTC GATTGCTCAG TCAAGAAGAT
30

(2) INFORMATION FOR SEQ ID NO:50:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

5

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..22

(D) OTHER INFORMATION: /product= "BB6300 oligomer"

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AAACAAACAAG AGGTTGGAGT GT

22

15

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

20

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

25

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..25

(D) OTHER INFORMATION: /product= "BB6381 oligomer"

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GAAGAAGTTT CABAGTAGTC AGCAA

35

25

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 25 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- 10 (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /product= "BB6302 oligomer"

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GTGGAATTTG AGAAGAGGTG TAAGA

25

(2) INFORMATION FOR SEQ ID NO:53:

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - 25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

30 (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /product= "BB6303 oligomer"

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GTAGTCAGCA GTGTTATTT GTGGAAT

27

40

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

10

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /product= "BB6625 oligomer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

20 TTTCAAAGTA GRCAGCAATG AAATT

25

(2) INFORMATION FOR SEQ ID NO:55:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /product= "BB6301 oligomer"

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

AGGTGTAAGA TTGACAAACAA GCGG

24

(2) INFORMATION FOR SEQ ID NO:56:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA

15

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /product= "BB6382 oligomer"

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

AGTAGTCAGC ABTGAAATTT TGTGG

25

25

(2) INFORMATION FOR SEQ ID NO:57:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: DNA

40

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /product= "BB6383 oligomer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TAGTCAAGAA TCTGACACCT GGCT

5 24

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- 20 (A) NAME/KEY: misc_feature
(B) LOCATION: 1..26
(D) OTHER INFORMATION: /product= "BB6384 oligomer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

25 GCACAGACTT GTTCCGAGCG CTTAGT
26

(2) INFORMATION FOR SEQ ID NO:59:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

40 (ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1..35
(D) OTHER INFORMATION: /product= "BB6385 oligomer"

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

AATTCCAAGT TAGAACATA TTGTTGAACC CATTC

35

10

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

20

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1..25
25 (D) OTHER INFORMATION: /product= "BB6345 oligomer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

30

GAAGAAAGTTT CTTCGTAGTC AGCAA

25

(2) INFORMATION FOR SEQ ID NO:61:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- 5 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..27
 (D) OTHER INFORMATION: /product= "BB7015 oligomer"

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

TGAGAAGAAG TTTCTTCGTA GTCAGCA

27

15 (2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

25

(ix) FEATURE:

- 30 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..27
 (D) OTHER INFORMATION: /product= "BB9112 oligomer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

TTGAACCCAG CGGCGAGATG GGTCAGC

35 27

(2) INFORMATION FOR SEQ ID NO:63:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- 10 (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /product= "BB9109 oligomer"

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

24 TTGAGAAGAA GTTCTAAAGT AGTC

20 (2) INFORMATION FOR SEQ ID NO:64:

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

30 (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /product= "BB9110 oligomer"

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ATTTGTGGA ATTTCTCTAG AGGT

24

40

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

10

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /product= "BB9111 Oligomer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

20 ATTTTGTGGA ATTCAGAAG AGGTGTAAGA

30

(2) INFORMATION FOR SEQ ID NO:66:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- 35
- (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..30
 - (D) OTHER INFORMATION: /product= "BB9104 Oligomer"

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

AGCAGCCAAG GAAGCAGATC TTTTATCCAA

30

(2) INFORMATION FOR SEQ ID NO:67:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA

15

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: /product= "BB9105 Oligomer"

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GTCAGCAGCC AATGGAGCAG ACAATCTTT ATCCAA

36

25

(2) INFORMATION FOR SEQ ID NO:68:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

35

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /product= "BB9106 oligomer"

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

TGGAGTGTCA GCTCTTTAT CCAA

5 24

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- 20 (A) NAME/KEY: misc_feature
(B) LOCATION: 1..30
(D) OTHER INFORMATION: /product= "BB9103 oligomer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

25 GTCAGCAGCC AATGGAGCTC TTTTATCCAA
30

(2) INFORMATION FOR SEQ ID NO:70:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

40 (ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1..48
(D) OTHER INFORMATION: /product= "BB9108 oligomer"

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

ACAGACTTGT CTACCGCGCT TAGTCAAGAA GATGACAGAT GGCTTGGA

48

10

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

20

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1..24
(D) OTHER INFORMATION: /product= "BB9107 oligomer"

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

30 AATTGTCTA GAGAAGTAAG AGAA

24

(2) INFORMATION FOR SEQ ID NO:72:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- 5 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..21
 (D) OTHER INFORMATION: /product= "BB9512 oligomer"

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

CAGCACAGAC AGATCTCGAG C

21

15 (2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

25

(ix) FEATURE:

- 30 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..18
 (D) OTHER INFORMATION: /product= "BB9432 oligomer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

CAAAGTAGGA AGCAATGA

35 18

(2) INFORMATION FOR SEQ ID NO:74:

38 (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 19 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA

10 (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /product= "BB9519 oligomer"

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GTGTAAGAGG CACAACAAAG

19

20 (2) INFORMATION FOR SEQ ID NO:75:

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

30 (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /product= "BB9527 oligomer"

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GAAGTTTCAG CGTAGTCAG

19

40

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

10

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /product= "BB9431 oligomer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

20 GTAGTCAGCA GCGAAATTT G

21

(2) INFORMATION FOR SEQ ID NO:77:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /product= "BB9534 oligomer"

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GTCAAGAAGG CGACACCTG

19

(2) INFORMATION FOR SEQ ID NO:78:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA

15

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /product= "BB9437 oligomer"

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CACAGACTTG AGACGAGCGC T

21

25

(2) INFORMATION FOR SEQ ID NO:79:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: DNA

40

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /product= "BB9433 oligomer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

GAGAAGAAGT AGAAAAGTAG TC

5 22

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- 20 (A) NAME/KEY: misc_feature
(B) LOCATION: 1..21
(D) OTHER INFORMATION: /product= "BB9506 oligomer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

25 TTTGTGGAAT AGATCTAGAG G
21

(2) INFORMATION FOR SEQ ID NO:81:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

40 (ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1..23
(D) OTHER INFORMATION: /product= "BB10194 oligomer"

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GGTTGGAGTG CGAGCAGCCA AGG

23

10

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

20

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1..22
(D) OTHER INFORMATION: /product= "BB10195 oligomer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

30 GGAATTTGTT CAGAGGTGTA AG

22

(2) INFORMATION FOR SEQ ID NO:83:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- 5 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..27
 (D) OTHER INFORMATION: /product= "BB10196 oligomer"

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GCACAGACTT GTCTTCGCG CTTAGTC

27

15 (2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
20 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

25

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..29
 (D) OTHER INFORMATION: /product= "BB10197 oligomer"

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GGAGTGTCAG CAGCTTCGGA TCTTTATC

35 29

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 22 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /product= "BB10198 oligomer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

15 GGAGTGTCAG CTTCCAAGGA TC
22

(2) INFORMATION FOR SEQ ID NO:86:

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA

- 30 (ix) FEATURE:
- (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..23
 - (D) OTHER INFORMATION: /product= "BB10199 oligomer"

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GGTTGGAGTG TCTTCAGCCA AGG

23

40

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

10

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /product= "BB10200 oligomer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

20 GGAATTTCTT CAGAGGTGTA AG

22

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /product= "BB10201 oligomer"

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CCTTATTAGG CAGATTCTTC CAAGTCAG

28

(2) INFORMATION FOR SEQ ID NO:89:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA

15

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /product= "BB9537 oligomer"

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GACTTGTCTA GCGCGCTTAG

20

25

(2) INFORMATION FOR SEQ ID NO:90:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

35

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /product= "BB9497 oligomer"

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GTCAGCAGCA GCGGATCTT

5 19

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- 20 (A) NAME/KEY: misc_feature
(B) LOCATION: 1..17
(D) OTHER INFORMATION: /product= "BB9498 oligomer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

25

GTCAGCAGAC AAGGATC

17

(2) INFORMATION FOR SEQ ID NO:92:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

40

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1..18
(D) OTHER INFORMATION: /product= "BB9499 oligomer"

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GAGTGTCAAGA AGCCAAGG

18

10

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

20

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1..22
(D) OTHER INFORMATION: /product= "BB9517 oligomer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

30

ATTAGGCAGA GGCTTCCAAG TC

22

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- 5 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..34
 (D) OTHER INFORMATION: /product= "BB9781 oligomer"

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

GAGAAACAAAC AAGCGGTAGA TCTTTATCC AAGC
34

15 (2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

25

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..20
 (D) OTHER INFORMATION: /product= "BB9430 oligomer"

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GTTGGAGTGG AAGCAGCAA

35 20

(2) INFORMATION FOR SEQ ID NO:96:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- 10 (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /product= "BB9525 oligomer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

15 CAGCAATGGC ATTTTGTG
18

(2) INFORMATION FOR SEQ ID NO:97:

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - 25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- 30 (ix) FEATURE:
- (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..21
 - (D) OTHER INFORMATION: /product= "BB9435 oligomer"

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GTCTCGAGCG AGAAGTCAAG A

21

40

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

10

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /product= "BB9436 oligomer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

20 GTCTCGAGGA CTTAGTCA

18

(2) INFORMATION FOR SEQ ID NO:99:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /product= "BB9423 oligomer"

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GAACCCATTC AGAAGATGGG TC

22

(2) INFORMATION FOR SEQ ID NO:100:

5

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA

15

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /product= "BB9424 oligomer"

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

TTTGAACCCA AGATTCA GAT G

21

25

(2) INFORMATION FOR SEQ ID NO:101:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: DNA

40

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /product= "BB9425 oligomer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

CAGAAACATA AGATTGAACC C

5 21

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- 20 (A) NAME/KEY: misc_feature
(B) LOCATION: 1..20
(D) OTHER INFORMATION: /product= "BB9427 oligomer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

25 CAATTCCAAG GAAGAACAT
20

(2) INFORMATION FOR SEQ ID NO:103:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

40 (ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1..17
(D) OTHER INFORMATION: /product= "BB9503 oligomer"

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

CCTTATTAGT CAGAAC

17

10

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

20

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1..33
(D) OTHER INFORMATION: /product= "BB9443 oligomer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

30 TTGAGAAGAA GTTCTAAAGT AGGCAGCAAT GAA

33

(2) INFORMATION FOR SEQ ID NO:105:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

5

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /product= "BB9434 oligomer"

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GACACCTGGA GAGGAACATT

20

15

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

25

(ix) FEATURE:

30

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /product= "BB9228 oligomer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

CAGACAATTG AGCGTCAGAA AC

35

22

(2) INFORMATION FOR SEQ ID NO:107:

40

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA

 (ix) FEATURE:

- 10 (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /product= "BB9429 oligomer"

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

 GGCAGACAAA GACAAGTCAG

20

20 (2) INFORMATION FOR SEQ ID NO:108:

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

 (ii) MOLECULE TYPE: DNA

30 (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /product= "BB9495 oligomer"

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

 CTTATTAGGA AGACAATTC

19

40

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- 5 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

10

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..19
- 15 (D) OTHER INFORMATION: /product= "BB9496 oligomer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

20 CAGCCAAGGC TCTTTATC

19

(2) INFORMATION FOR SEQ ID NO:110:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- 35 (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /product= "BB9509 oligomer"

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

CTTGGAACAA GAAGAAGAAG

20

(2) INFORMATION FOR SEQ ID NO:111:

5

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA

15

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..19

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GTCAGAAACA GCTTTTG

19

25

(2) INFORMATION FOR SEQ ID NO:112:

30

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

35

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /product= "BB9529 oligomer"

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CATTGAGAAG CAGTTCAA

19

5

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

15

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /product= "BB9530 oligomer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

25 GAACATTGAG CAGAAGTTT

19

(2) INFORMATION FOR SEQ ID NO:114:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION: 1..21
(D) OTHER INFORMATION: /product= "BB9536 oligomer"

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GCGCTTAGTA GCGAAGATGA C
21

10 (2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

20

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..22
(D) OTHER INFORMATION: /product= "BB9422 oligomer"

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

CTTCAGATGG AGAACGACAG AC

30 22

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /product= "BB9426 oligomer"

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

10 CAAGTCAGAA GCATATTTT G

21

(2) INFORMATION FOR SEQ ID NO:117:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- 25
- (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..17
 - (D) OTHER INFORMATION: /product= "BB9504 oligomer"

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GGTGTAAGCG AAACAAAC

17

35 (2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

40

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

5

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /product= "BB9505 oligomer"

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

ATTTGTCTAG CGGTGTAAG

15

19

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /product= "BB9507 oligomer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

35

GAAATTTGA GCAATTGTC

20

(2) INFORMATION FOR SEQ ID NO:120:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: DNA

10

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /product= "BB9510 oligomer"

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

CTGGCTTGGC ACATTGAG

18

20

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: DNA

30

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /product= "BB9514 oligomer"

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

40

GAAACATATT TAGAAACCCA TTC

23

(2) INFORMATION FOR SEQ ID NO:122:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA

15 (ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..19

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

ATTAAGGCAGC CAATTCCAA

19

25 (2) INFORMATION FOR SEQ ID NO:123:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA

- 35 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..19
 (D) OTHER INFORMATION: /product= "BB9520 oligomer"

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

CTAGAGGTGG CAGAGAAC

19

5

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

15

(ix) FEATURE:

- 20 (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /product= "BB9522 oligomer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

25 TTTTGTGGAG CTTGTCTAG

19

(2) INFORMATION FOR SEQ ID NO:125:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- 40 (A) NAME/KEY: misc_feature

(B) LOCATION: 1..20
(D) OTHER INFORMATION: /product= "BB9531 oligomer"

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

GATGACACCA GCCTTCCAAC

20

10 (2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

20

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /product= "BB9532 oligomer"

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GAAGATGACA GCTGGCTTGG

30 20

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /product= "BB9533 oligomer"

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

10 AGAAGATGGC ACCTGGCT

18

(2) INFORMATION FOR SEQ ID NO:128:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- 25
- (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..17
 - (D) OTHER INFORMATION: /product= "BB9500 oligomer"

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

GGTTGGAGCG TCAGCAG

17

35 (2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

40

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

5

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /product= "BB9523 oligomer"

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

CAATGAAATT AGATGGAATT TG

15

22

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

30

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /product= "BB9511 oligomer"

35

GCGCTTAGCC AAGAAGA

17

(2) INFORMATION FOR SEQ ID NO:131:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- 5 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

10 (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /product= "BB9501 oligomer"

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

CAAGCGGTAG CAGTGTAG

19

20

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- 25 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

30

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..18
- 35 (D) OTHER INFORMATION: /product= "BB9502 oligomer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

40 ACAAGCGGCT GGAGTGTC

18

(2) INFORMATION FOR SEQ ID NO:133:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA

15 (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /product= "BB9508 oligomer"

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

GTTTCAAAGG CGTCAGCA

18

25 (2) INFORMATION FOR SEQ ID NO:134:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA

35

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /product= "BB9513 oligomer"

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

TTCTTCAGAT GCGTCAGCAC

5 20

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- 20 (A) NAME/KEY: misc_feature
(B) LOCATION: 1..18
(D) OTHER INFORMATION: /product= "BB9516 oligomer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

25 CAAGTCAGCA ACATATT
18

(2) INFORMATION FOR SEQ ID NO:136:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

40 (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1..17
(D) OTHER INFORMATION: /product= "BB9521 oligomer"

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GTCTAGAGGC GTAAGAG

17

10

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

20

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1..17
25 (D) OTHER INFORMATION: /product= "BB9524 oligomer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

30 CAATGAAAGA TTGTGGAA

18

(2) INFORMATION FOR SEQ ID NO:138:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- 5 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..17
 (D) OTHER INFORMATION: /product= "BB9526 oligomer"

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

GTAGTCAGAA ATGAAAT

17

15

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

25

(ix) FEATURE:

- 30 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..18
 (D) OTHER INFORMATION: /product= "BB9528 oligomer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

35 GAGAAGAAGC TTCAAAGT

18

(2) INFORMATION FOR SEQ ID NO:140:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- 10 (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /product= "BB9535 oligomer"

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

CTTAGTCAAG GCGATGACAC

20

20 (2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

30

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /product= "BB9538 oligomer"

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GTCAGCACAG GCTTGTCTCG

40

20

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

10

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /product= "BB9539 oligomer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

20 TGGGTCAGAA CAGACTT

17

(2) INFORMATION FOR SEQ ID NO:143:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /product= "BB9540 oligomer"

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

CATTCAG CTGGGTCA

19

(2) INFORMATION FOR SEQ ID NO:144:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA

15

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /product= "BB9541 oligomer"

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

ATTTTGAAAC AGCTTCTTCA

20

25

(2) INFORMATION FOR SEQ ID NO:145:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

35

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /product= "BB9542 oligomer"

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

CATATTTTG AGCCCATTCT TC

5 22

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- 20 (A) NAME/KEY: misc_feature
(B) LOCATION: 1..21
(D) OTHER INFORMATION: /product= "BB10374 oligomer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

25 TTTTGAACC AATTCTTCAG A
21

(2) INFORMATION FOR SEQ ID NO:147:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

40 (ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1..21
(D) OTHER INFORMATION: /product= "BB10375 oligomer"

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

CAGAAACATA ATCTTGAACC C

21

10

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

20

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1..19
(D) OTHER INFORMATION: /product= "BB10376 oligomer"

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

30 GTCAGAAACA TCTTTTGA

19

(2) INFORMATION FOR SEQ ID NO:149:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- 5 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..19
 (D) OTHER INFORMATION: /product= "BB10377 oligomer"

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

GTGTAAGAAT CACAACAAG

19

15 (2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

25

(ix) FEATURE:

- 30 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..23
 (D) OTHER INFORMATION: /product= "BB11235 oligomer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GAAACAAACAA GCTTCTGGAG TGT

35 23

(2) INFORMATION FOR SEQ ID NO:151:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- 10 (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /product= "BB10379 oligomer"

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

ATTAGGCTTC CAATTCAA
19

20 (2) INFORMATION FOR SEQ ID NO:152:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

30 (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /product= "BB10380 oligomer"

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

ATTAGGCAGA ATCTTCCAAG TC

22

40

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

10

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /product= "BB10381 oligomer"

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

20 CAATTCCAAT CTAGAACAT

20

(2) INFORMATION FOR SEQ ID NO:154:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /product= "BB10382 oligomer"

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

CATTGAGATT CAGTTCAA

19

(2) INFORMATION FOR SEQ ID NO:155:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA

15

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /product= "BB10383 oligomer"

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GTCAAGAACGT TGACACCTG

19

25

(2) INFORMATION FOR SEQ ID NO:156:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

35

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /product= "BB10964 oligomer"

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GCGCTTAGTG TTGAAGATGA C

5 21

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- 20 (A) NAME/KEY: misc_feature
(B) LOCATION: 1..27
(D) OTHER INFORMATION: /product= "BB10385 oligomer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

25 GTAAAGAGAAA CATTGACAAG CGGTTGG
27

(2) INFORMATION FOR SEQ ID NO:158:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

40 (ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1..24
(D) OTHER INFORMATION: /product= "BB10386 oligomer"

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

TTGAACCCAT TGTTGAGATG GGTC

24

10

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- 25 (A) NAME/KEY: misc_feature
(B) LOCATION: 1..21
(D) OTHER INFORMATION: /product= "BB10529 oligomer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

30

GTTTCAAAGT ATTGAGCAAT G

21

(2) INFORMATION FOR SEQ ID NO:160:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
40 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

5

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..26

(D) OTHER INFORMATION: /product= "BB10530 oligomer"

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

GATGACACCT GGTCGGAAC ATTGAG

26

15

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

20

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

25

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..26

(D) OTHER INFORMATION: /product= "BB10531 oligomer"

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

CTTGTCTCGA GCGTTCAAGTC AAGAAG

35

26

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 25 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- 10 (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /product= "BB10532 oligomer"

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

25 GACTTGTCTC GATTCCCTAG TCAAG

25

(2) INFORMATION FOR SEQ ID NO:163:

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - 25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- 30 (ix) FEATURE:
- (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..27
 - (D) OTHER INFORMATION: /product= "BB10533 oligomer"

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

CCATTCTTCA GATGGTGGAG CACAGAC

27

40

(2) INFORMATION FOR SEQ ID NO:164:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA

15 (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /product= "BB10534 oligomer"

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

25 GCAGACAATT GCAAGTCAG

19

20 (2) INFORMATION FOR SEQ ID NO:165:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA

35 (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /product= "BB10535 oligomer"

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

GTAGTCAGCC AAGAAATTTT G

21

(2) INFORMATION FOR SEQ ID NO:166:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA

15

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..21
- (D) OTHER INFORMATION: /product= "BB10536 oligomer"

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

GTAGTCAGCG ACGAAATTTT G

21

25

(2) INFORMATION FOR SEQ ID NO:167:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

35

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /product= "BB10195 oligomer"

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

GGAATTTGTT CAGAGGTGTA AG

5 22

(2) INFORMATION FOR SEQ ID NO:168:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

20 (A) NAME/KEY: misc_feature

(B) LOCATION: 1..17

(D) OTHER INFORMATION: /product= "BB5769 primer"

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

GCATTCTGAC ATCCTCT

17

30 (2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

40

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..31
- (D) OTHER INFORMATION: /product= "BB6040 primer"

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

CGTTAAAATC AACAACTTGT CAATTGGAAC C

10

31

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /product= "BB6296 primer"

30

GGAAATCTCA CAGATCT

17

(2) INFORMATION FOR SEQ ID NO:171:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

5

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /product= "BB8461 primer"

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

GAAGGAAATC TCATCGTTG AATA

24

15

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

25

(ix) FEATURE:

30

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /product= "BB8740 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

GCTAATGCGG AGGATGC

35

17

(2) INFORMATION FOR SEQ ID NO:173:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- 10 (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..31
- (D) OTHER INFORMATION: /product= "BB6394 primer"

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

CCGGCATTAC AACTTATCGA TAAGCTTGCA C
31

20 (2) INFORMATION FOR SEQ ID NO:174:

- 25 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- 30 (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..17
 - (D) OTHER INFORMATION: /product= "BB6037 primer"

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GCGCATTGTT AGATTTC

17

40

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

10

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /product= "BB6841 primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

20 CTTATCGATC AACTTGCACA AACG

24

(2) INFORMATION FOR SEQ ID NO:176:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- 35
- (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..28
 - (D) OTHER INFORMATION: /product= "BB6189 primer"

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

GTCATGTCTA AGGCGGATCC TTATTAAC

28

(2) INFORMATION FOR SEQ ID NO:177:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: cDNA

15

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..24
- (D) OTHER INFORMATION: /product= "BB8661 primer"

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GAGAATGGCA ACAACTTATG CATT

24

25

(2) INFORMATION FOR SEQ ID NO:178:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

35

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /product= "BB6038 primer"

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

CCAACATCAA TACAACC

5 17

CLAIMS

1. A proteinaceous molecule with stem cell inhibition (SCI) activity, the molecule being substantially incapable at physiological ionic strength of forming a stable multimer higher than a dodecamer.
5
2. A molecule as claimed in claim 1, which is substantially incapable at physiological ionic strength of forming a stable multimer higher than a tetramer.
10
3. A molecule as claimed in claim 2, which at physiological ionic strength forms a substantially homogeneous population of tetramers.
4. A molecule as claimed in claim 1, which is substantially incapable at physiological ionic strength of forming a stable multimer higher than a dimer.
15
5. A molecule as claimed in claim 1, which is substantially incapable at physiological ionic strength of forming a stable multimer higher than a monomer.
20
6. A molecule as claimed in any one of claims 1 to 5, which is an analogue of a natural SCI in which, relative to the natural SCI, one or more of the amino acid residues involved in promoting and/or stabilising association of the components of a dimeric tetrameric, dodecameric or higher order complex is altered to have a lesser promoting and/or stabilising effect.
25
7. A molecule as claimed in claim 6, wherein the natural SCI is LD78 or MIP-1 α .

8. A molecule as claimed in claim 6, wherein the alteration is a substitution.
9. A molecule as claimed in claim 8, wherein the substitution is such as to cause charge repulsion.
5
10. A molecule as claimed in claim 8, wherein a hydrophilic residue is substituted for a hydrophobic residue.
11. A molecule as claimed in claim 8, wherein a neutral residue is substituted for a charged residue.
10
12. A molecule as claimed in claim 6, wherein a small, weakly hydrophobic residue is substituted for a large, strongly hydrophobic residue.
13. A molecule as claimed in any one of claims 8 to 12, wherein the substitution takes place at one or more of residues 12 to 16 of LD78.
15
14. A molecule as claimed in claim 12, wherein the substitution is Ile19>Ala and/or Val39>Ala.
20
15. A molecule as claimed in any one of claims 8 to 11, wherein the substitution takes place at one or more of those residues projecting away from the surface of the dimer in strand 1 of the β sheet, and/or in the turn between strands 2 and 3 of the sheet.
25
16. A molecule as claimed in claim 15, wherein the substitution takes place between residues 24 to 29 (inclusive) of LD78 and/or 43 to 47 (inclusive) of LD78.

17. A molecule as claimed in claim 16, wherein the substitution is:
- (i) Ile24 > Asn;
(ii) Tyr27 > Asn;
(iii) Phe28 > Glu;
5 (iv) Glu29 > Arg;
(v) Lys44 > Glu (especially with Arg45 > Gln); and/or
(vi) Arg45 > Glu.
18. A molecule as claimed in any one of claims 8 to 12, wherein the substitution takes place in at least one of those residues which form a chain N-terminal to the turn into strand 1 of the sheet.
- 10
19. A molecule as claimed in any one of claims 1 to 8, which is an LD78 analogue having at least one of the following substitutions with respect to wild-type LD78: Lys44 > Glu (with Arg45 > Gln), Arg47 > Glu, Phe28 > Glu, Phe28 > Glu (with Gln48 > Glu), Phe28 > Glu (with Arg47 > Glu), Arg17 > Ser (with Gln18 > Glu), Phe12 > Ala, Val39 > Ala, Ile40 > Ala, Asp26 > Ala (with Glu29 > Arg and Arg47 > Glu), Arg17 > Ser, Glu29 > Arg, Gln18 > Glu, Asp26 > Ser, Gln48 > Ser, Thr15 > Ala, Gln21 > Ser, Phe23 > Ala, Ser32 > Ala, Ala51 > Ser, Ala4 > Glu, Phe12 > Asp, Asp26 > Gln, Lys36 > Glu, Lys44 > Glu, Arg45 > Glu, Glu66 > Gln, Phe12 > Gln, Lys44 > Ser, Arg17 > Glu (with Gln18 > Glu), Asp26 > Ala, Glu66 > Ser.
- 15
20. A molecule as claimed in any one of claims 1 to 8, which is an LD78 analogue having at least one of the following substitutions with respect to wild-type LD78: Arg17 > Ser, Glu29 > Arg, Gln18 > Glu, Asp26 > Ser, Gln48 > Ser, Thr15 > Ala, Gln21 > Ser, Phe23 > Ala, Ser32 > Ala, Ala51 > Ser, Ala4 > Glu, Phe12 > Asp, Asp26 > Gln, Lys36 > Glu,
- 25

Lys44>Glu, Arg45>Glu, Glu66>Gln, Phe12>Gln, Lys44>Ser,
Arg17>Glu (with Gln18>Glu), Asp26>Ala, Glu66>Ser.

21. A molecule as claimed in any one of claims 1 to 8, which is an LD78 analogue having at least one of the following substitutions with respect to wild-type LD78: Phe12>Gln, Lys44>Ser, Arg17>Glu (with Gln18>Glu), Asp26>Ala, Glu66>Ser.
- 5
22. A molecule as claimed in any one of claims 1 to 8, which is an LD78 analogue having at least one of the following substitutions with respect to wild-type LD78: Asp26>Ala, Glu66>Ser.
- 10
23. LD78 (Asp26>Ala).
- 15 24. LD78 (Glu66>Ser).
- 20
25. A molecule as claimed in any one of claims 1 to 12 which comprises a sequence substantially corresponding to LD78, but with a mutation at one or more (but preferably no more than two) of the following amino acid residues: Ser1, Leu2, Ala3, Ala4, Asp5, Thr6, Ala9, Phe12, Ser13, Tyr14, Ser16, Arg17, Gln18, Ile19, Pro20, Gln21, Phe23, Ile24, Asp26, Tyr27, Phe28, Glu29, Ser31, Ser32, Gln33, Ser35, Lys36, Pro37, Gly38, Val39, Ile40, Leu42, Thr43, Lys44, Arg45, Ser46, Arg47, Gln48, Asp52, Glu55, Glu56, Gln59, Lys60, Tyr61, Val62, Asp64, Leu65, Leu67, Glu66, Ser68 and Ala69.
- 25
26. A molecule as claimed in any one of claims 1 to 25, which is an LD78 analogue and which is free of any N-terminal extension preceding Ser-1.

27. A molecule as claimed in any one of claims 1 to 26, which is an LD78 analogue and which has an N-terminal deletion, relative to the wild type molecule, of from one to seven residues.

- 5 28. A molecule as claimed in any one of claims 1 to 12, which comprises a sequence substantially corresponding to MIP-1 α , but with a mutation at one or more (but preferably not more than two) of the following amino acid residues: Ala1, Pro2, Tyr3, Gly4, Ala5, Asp6, Thr7, Ala10, Phe13, Ser14, Tyr15, Ser16, Arg17, Lys18, Ile19, Pro20, Arg21, Phe23, Ile24, Asp26, Phe28, Glu29, Ser31, Ser32, Glu33, Ser35, Gln36, Pro37, Gly38, Val39, Ile40, Leu42, Thr43, Lys44, Arg45, Asn46, Arg47, Gln48, Asp52, Glu55, Thr56, Gln59, Glu60, Tyr61, Ile62, Asp64, Leu65, Glu66, Leu67, Asn68 and Ala69.

- 10 29. Nucleic acid coding for a protein as claimed in any one of claims 1 to 28.

- 15 30. Nucleic acid as claimed in claim 29, which is recombinant DNA in the form of a vector.

- 20 31. A host cell transfected or transformed with a vector as claimed in claim 30.

- 25 32. A compound as claimed in any one of claims 1 to 28 for use in medicine.

33. The use of a compound as claimed in any one of claims 1 to 28 in the preparation of an agent for use as a stem cell protective agent.

- 25 34. A pharmaceutical formulation comprising a compound as claimed in any one of claims 1 to 28 and a pharmaceutically acceptable carrier.

35. A process for producing a compound as claimed in any one of claims 1 to 28 by expression of nucleic acid as claimed in claim 29 in *S. cerevisiae*.
36. A process for producing a compound as claimed in any one of claims 1 to 28 by expression of nucleic acid as claimed in claim 29 in *P. pastoris*.
37. A process for the production of a molecule having stem cell inhibitor activity, the process comprising culturing a yeast of the genus *Pichia*, and preferably of the species *pastoris*, the yeast having expressible heterologous nucleic acid coding for the molecule.
38. A method of increasing protein expression levels in a system in which the desired protein normally forms soluble multimeric complexes at physiological ionic strength (the "multimeric protein"), which method comprises using in the expression system cells which are transformed or transfected with a vector comprising DNA coding, not for the multimeric protein, but instead for a mutant thereof which has a reduced tendency to form soluble multimeric complexes relative to the multimeric protein.
39. A method as claimed in claim 38, in which the protein has stem cell inhibitor activity.

FIG. 1A

LD78	-SLAAADTPPIA	CCFSYTSRK-I	EQNIIADYFE	ISSQCSKPGV	IFLILKRSRQV	49
ACT-2	APMGSBPEPA	CCFSYTTARKL	PRNIVVBDYIE	ISSSLISQEAIV	VFQIKRSRQV	50
MIP-1 Alpha	APYGADTPPIA	CCFSYTSRK-I	PROEIVDYFE	ISSSLISQPGV	IFLILKERNRQI	49
LD78	CADPSEENVIC	KIVVSDEELSA				69
ACT-2	CADPSESWVIC	EYVYDIEIN-				69
MIP-1 Alpha	CADSKEIWIC	EITIDIEINA				69

FIG. 1B

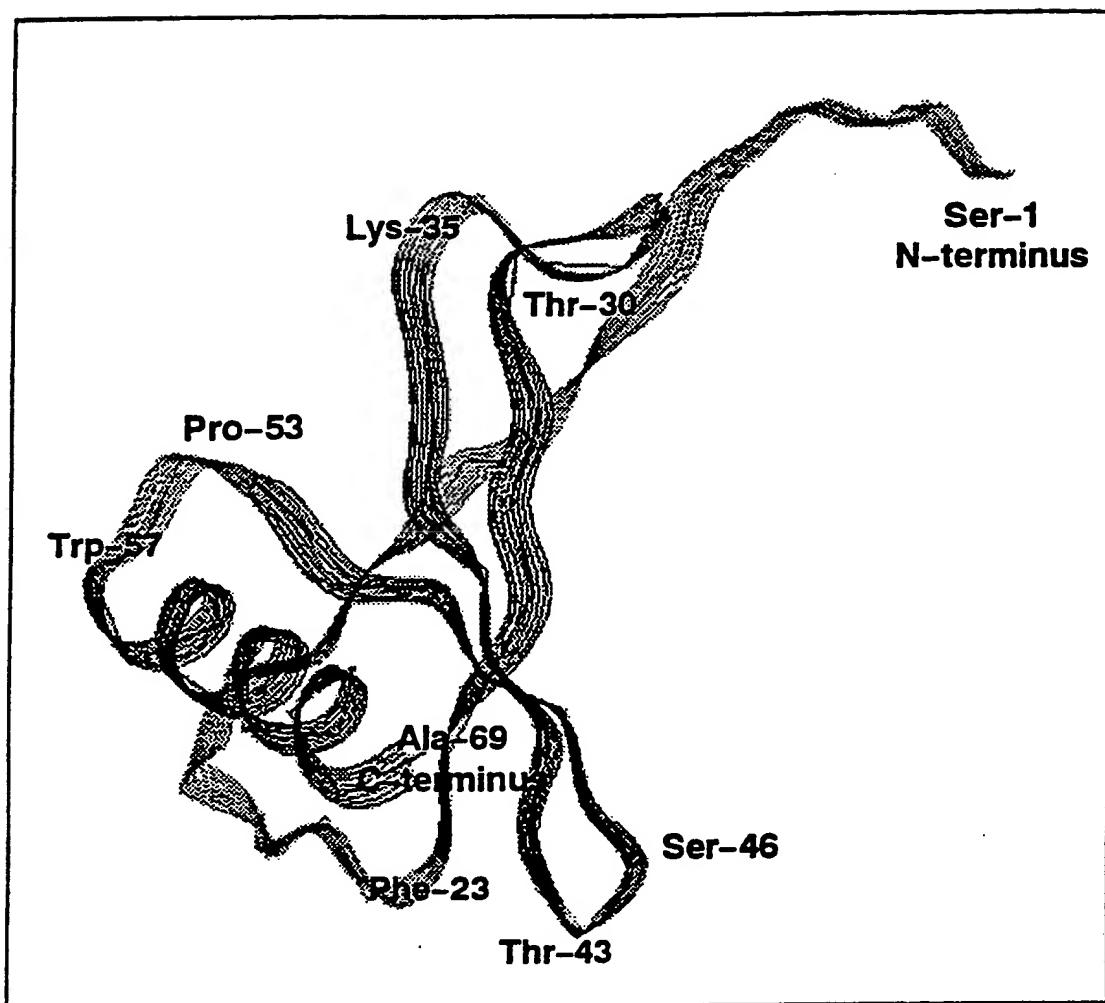
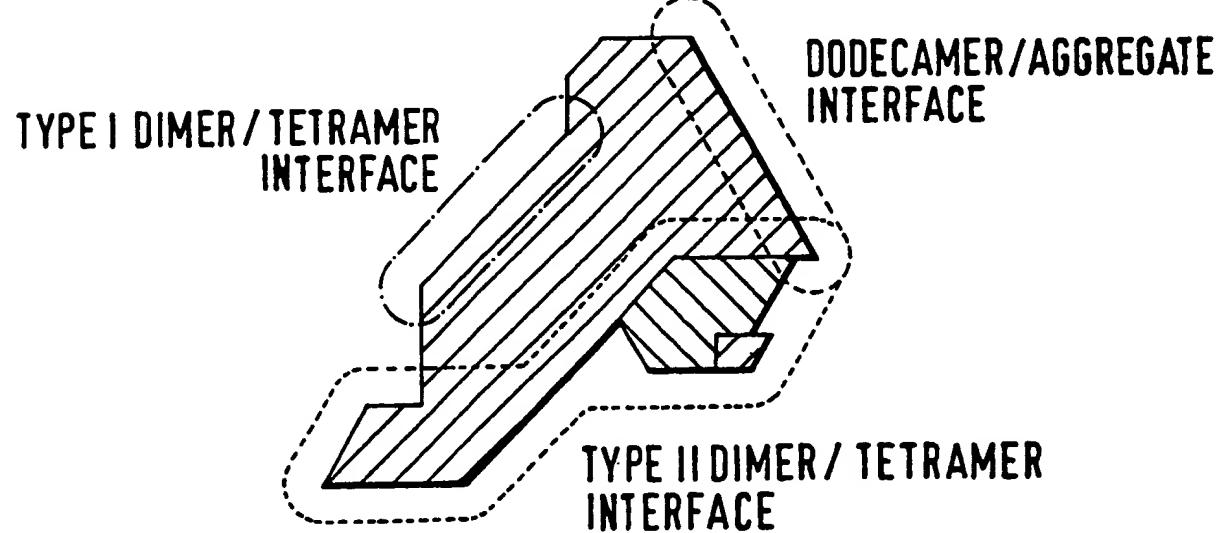


FIG. 1C



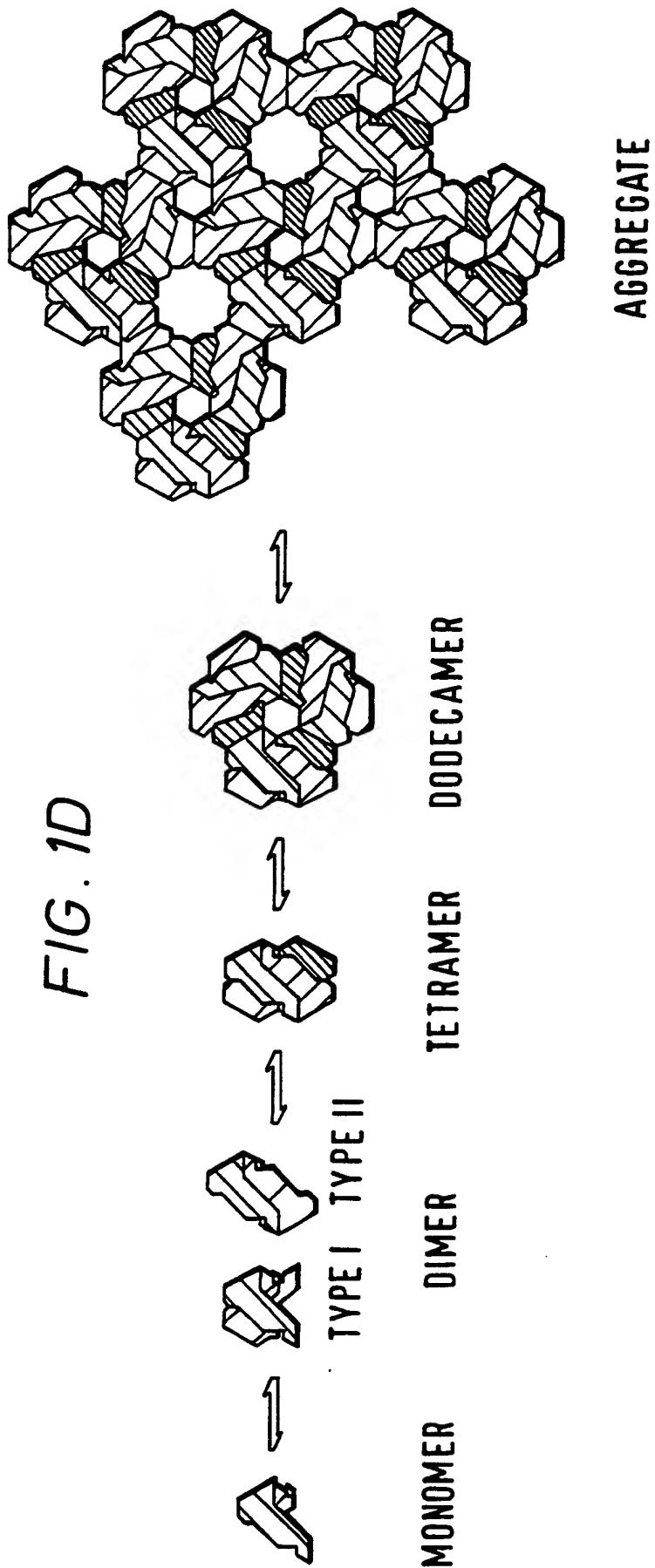
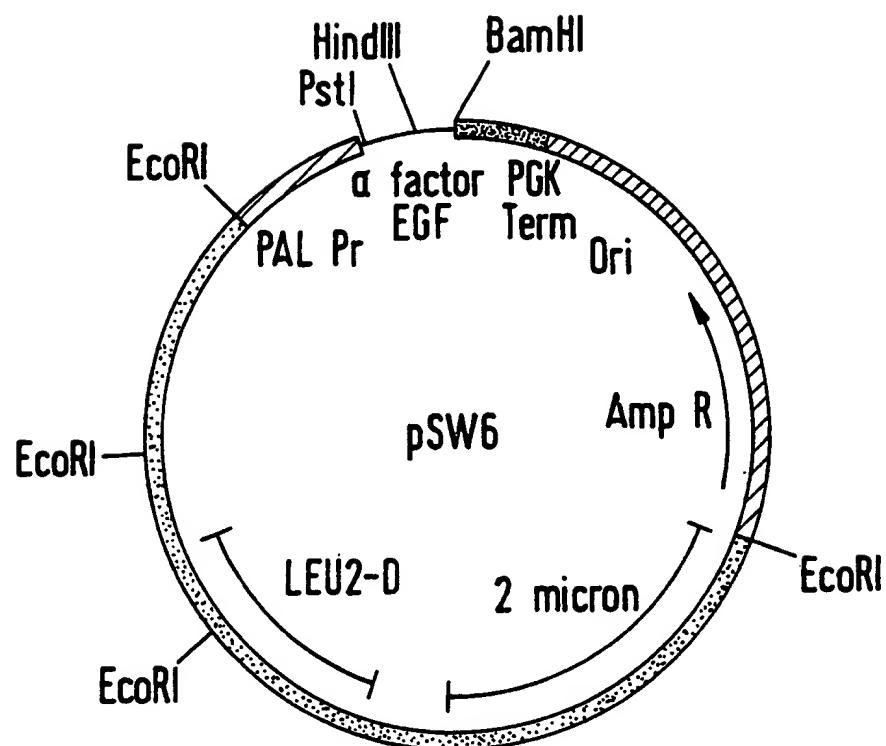


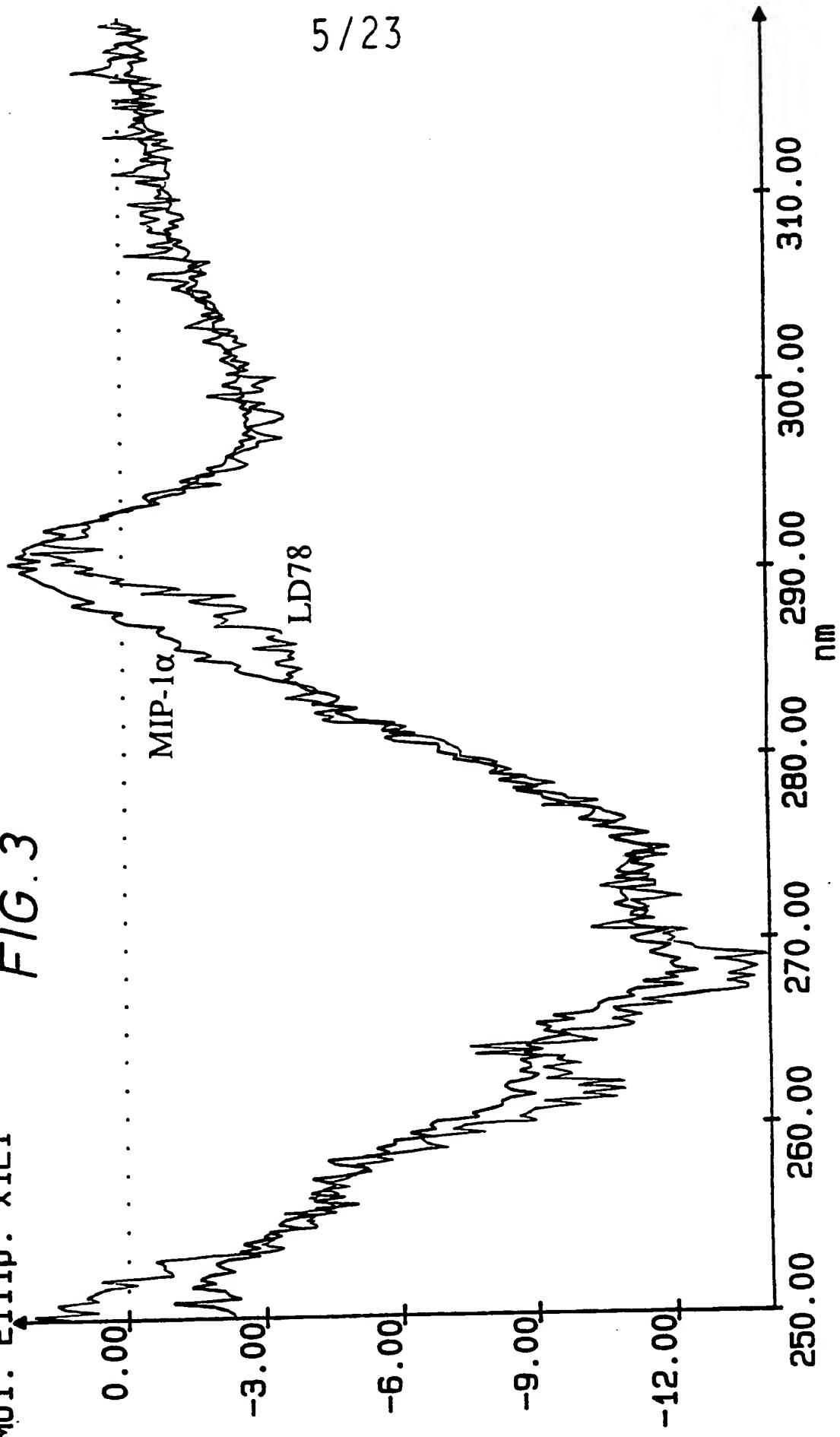
FIG. 1D

FIG. 2



Mol. Ellip. x1E1

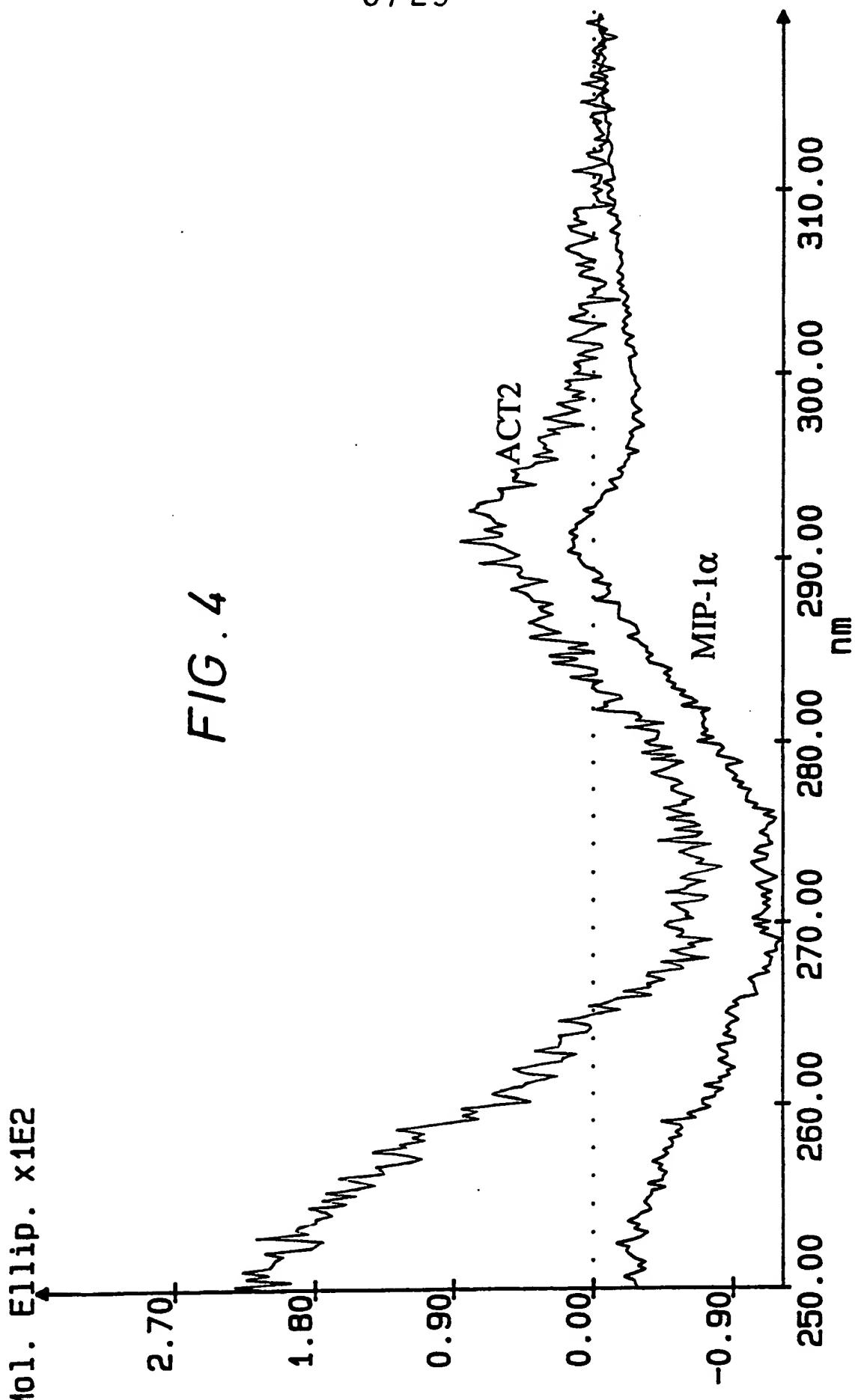
FIG. 3



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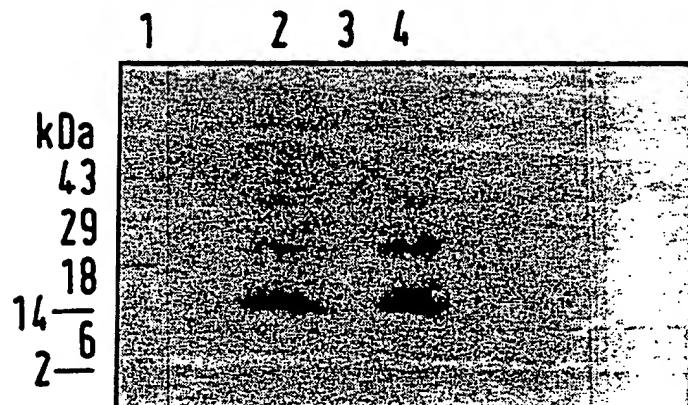
FIG. 4



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LANE	SAMPLE
1	markers
2	MIP-1a
3	Act-2
4	LD78

FIG. 5



LANE	SAMPLE
1	EGF
2	MIP-1a
3	Act-2
4	Ld78
5	markers

FIG. 7

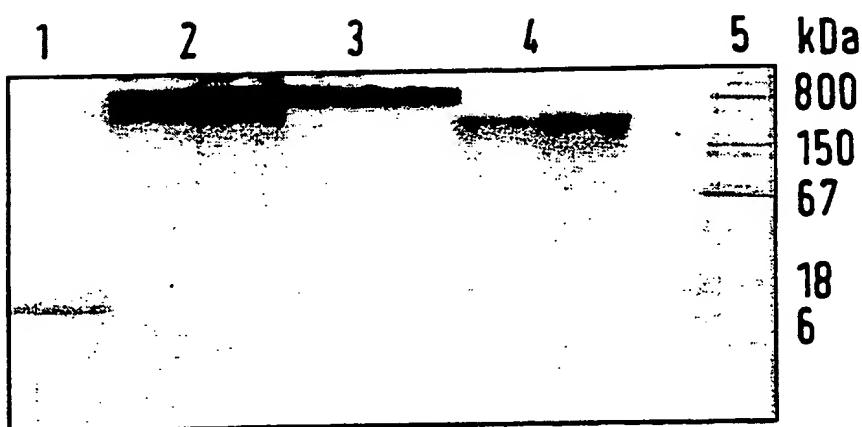
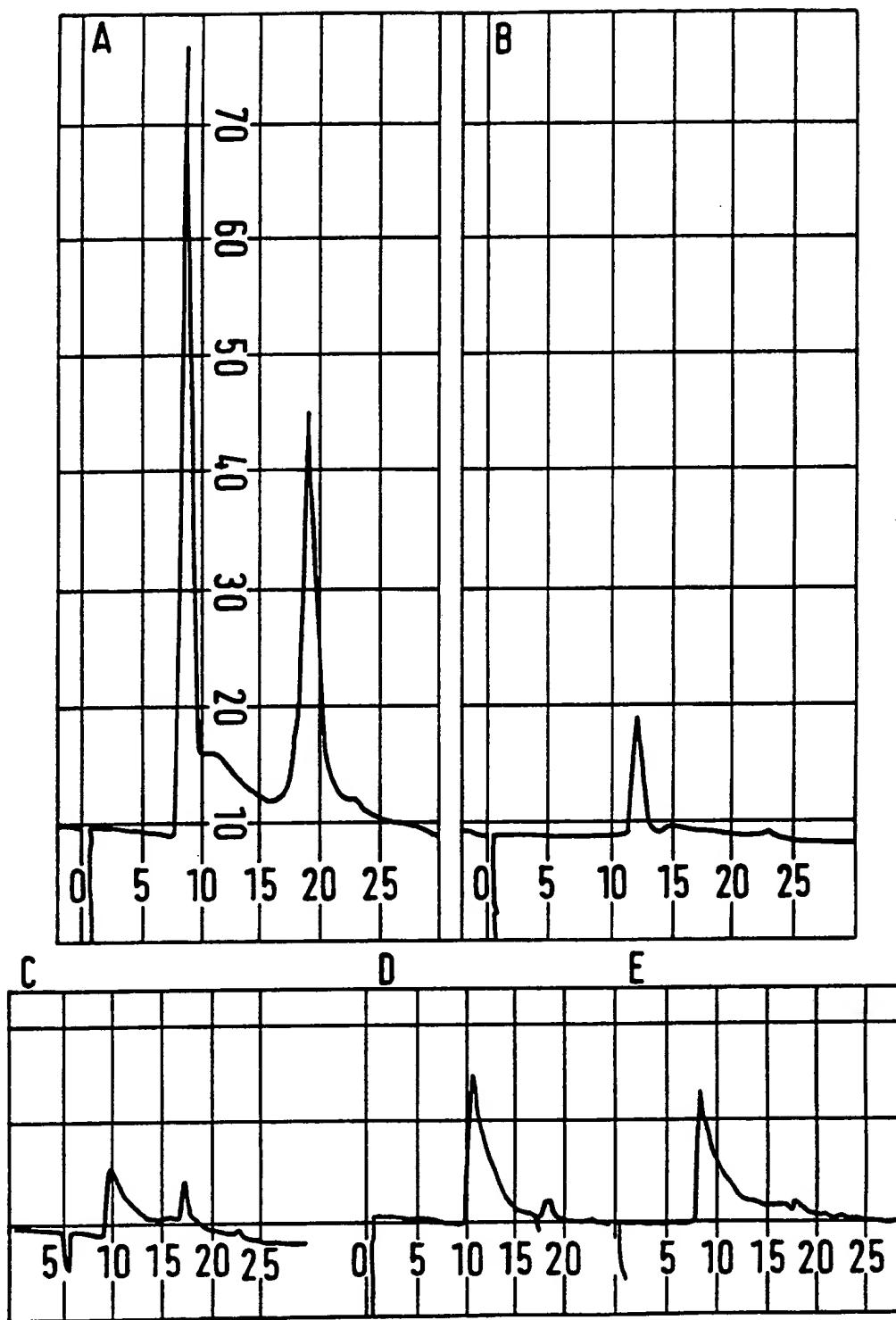
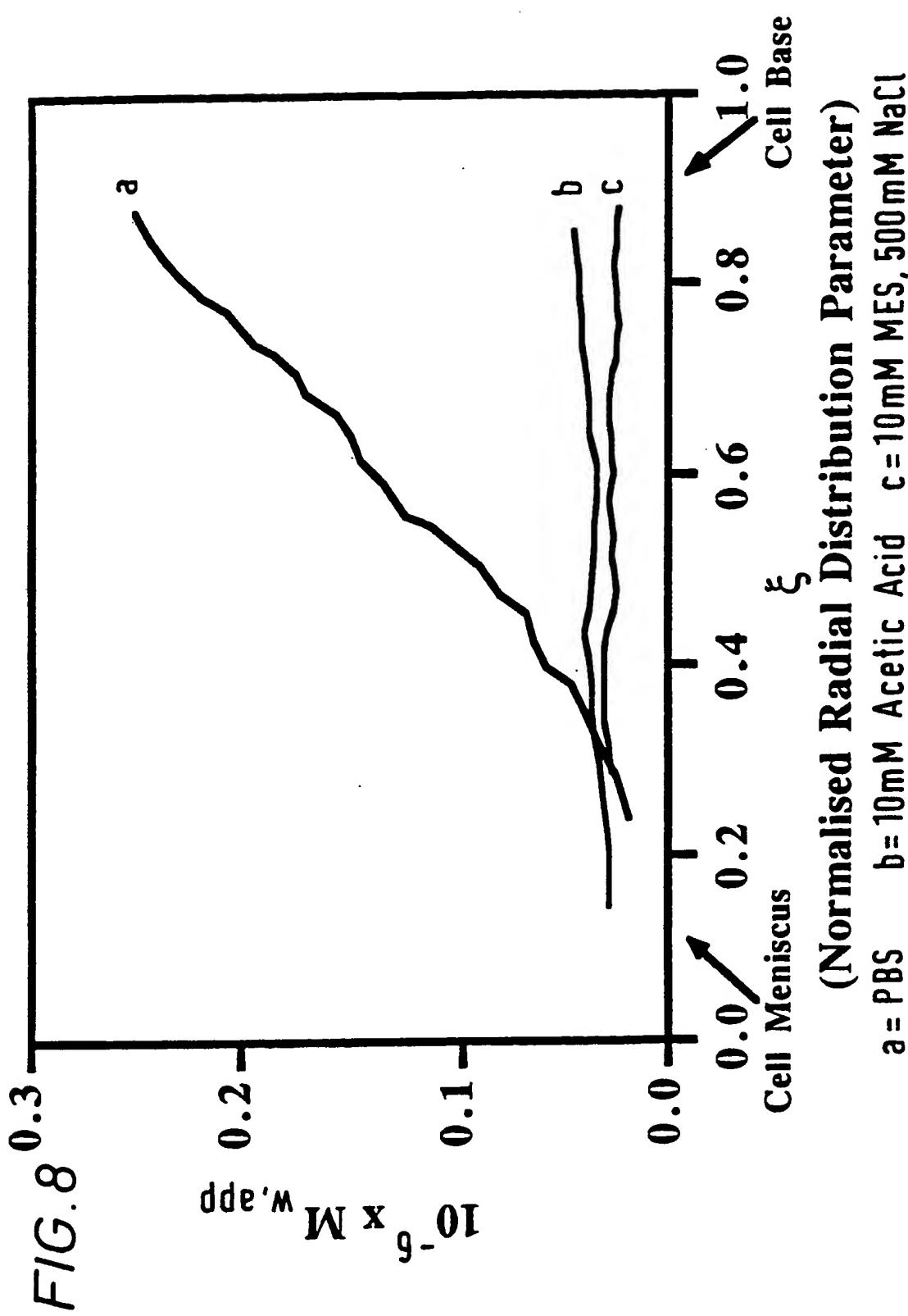


FIG.6

**A STANDARDS**

BLUE DEXTRAN	2000kD
LYSOZYME	14kD
ALDOLASE	158kD
MIP-1 α	500-800kD
L078	300-700kD
ACT-2	500-1000kD



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FIG. 9

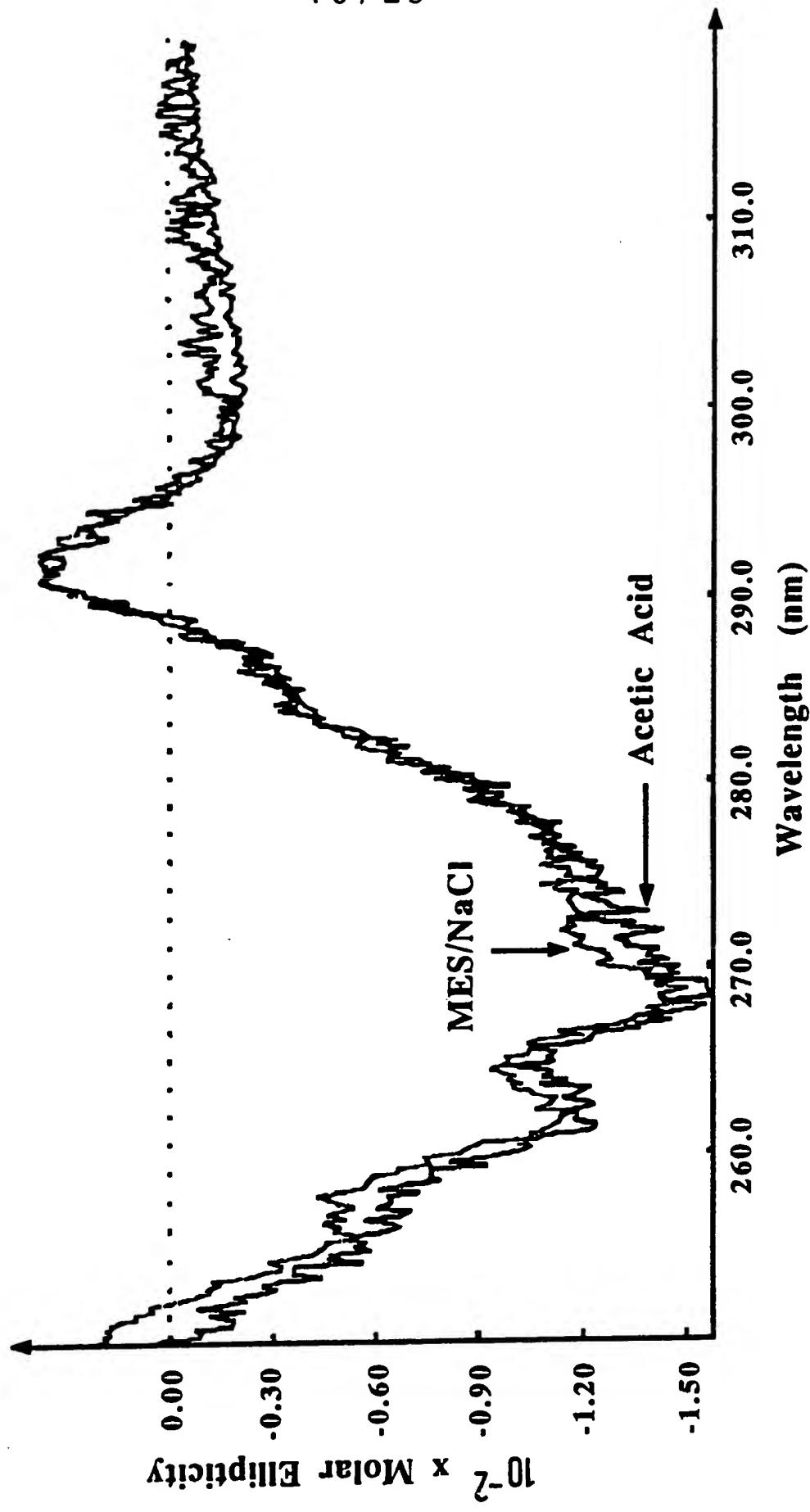


FIG. 10

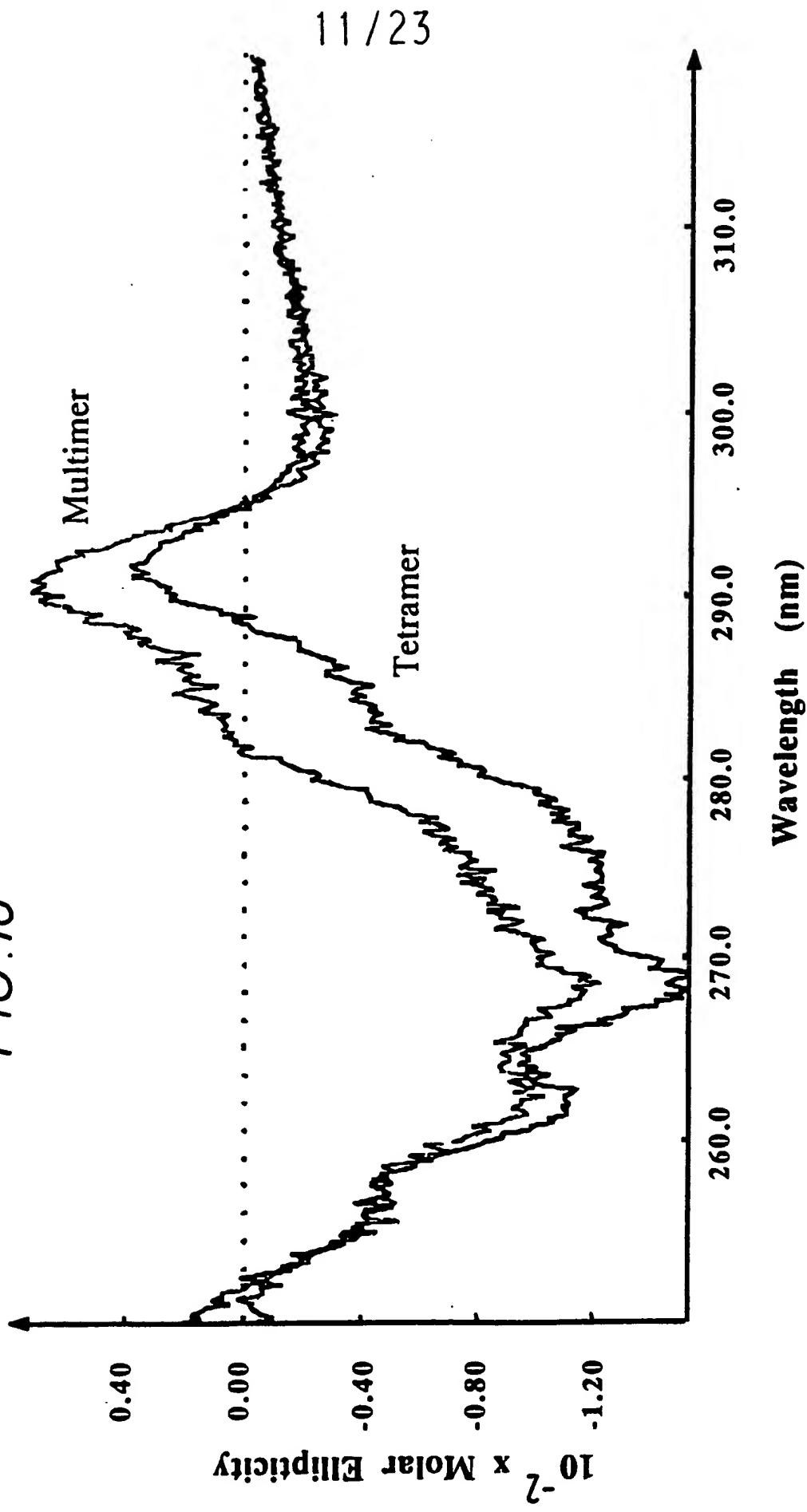


FIG. 11

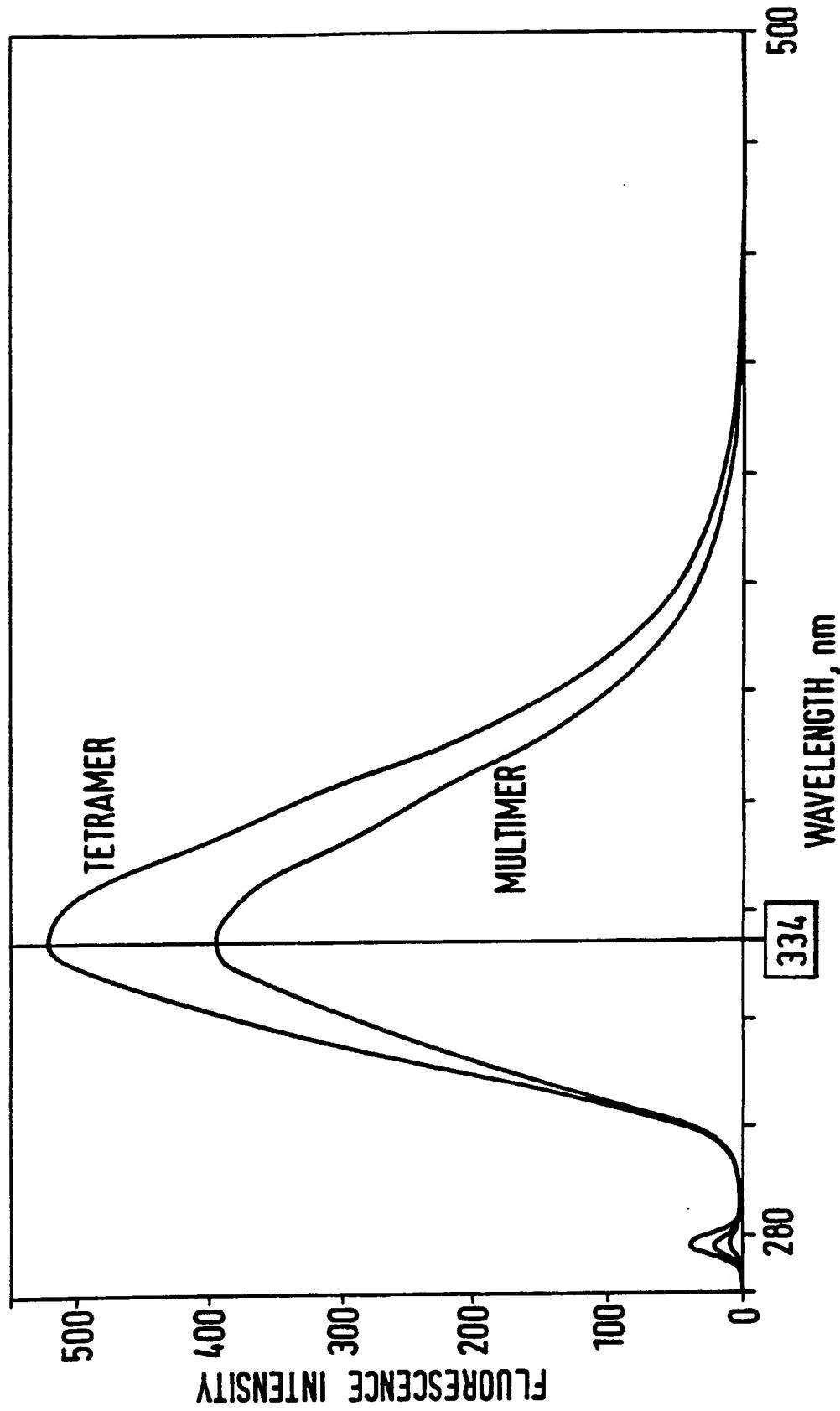
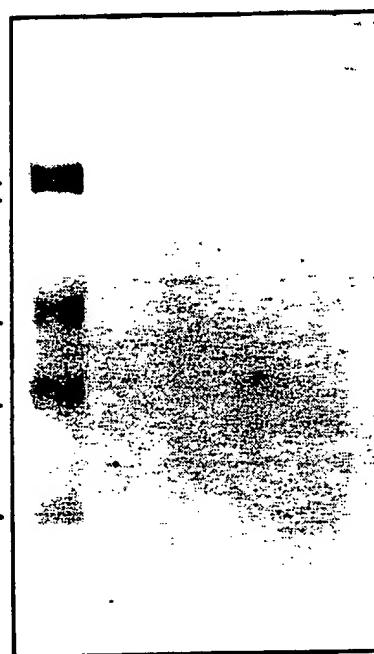


FIG. 12

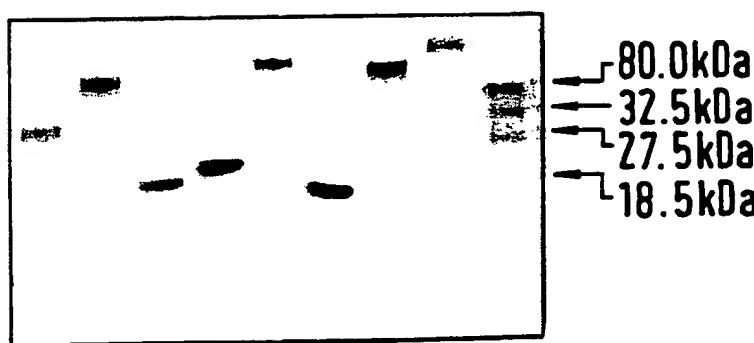
STDS WT M10 M11 M52

80kDa
49.5kDa
32.5kDa
27.5kDa
18.5kDa



Tracks from left
to right :

FIG. 13



Mutant 30
Mutant 29
Mutant 26
Mutant 15
Mutant 10
Mutant 2
Mutant 1
Wild type
Markers

FIG. 14

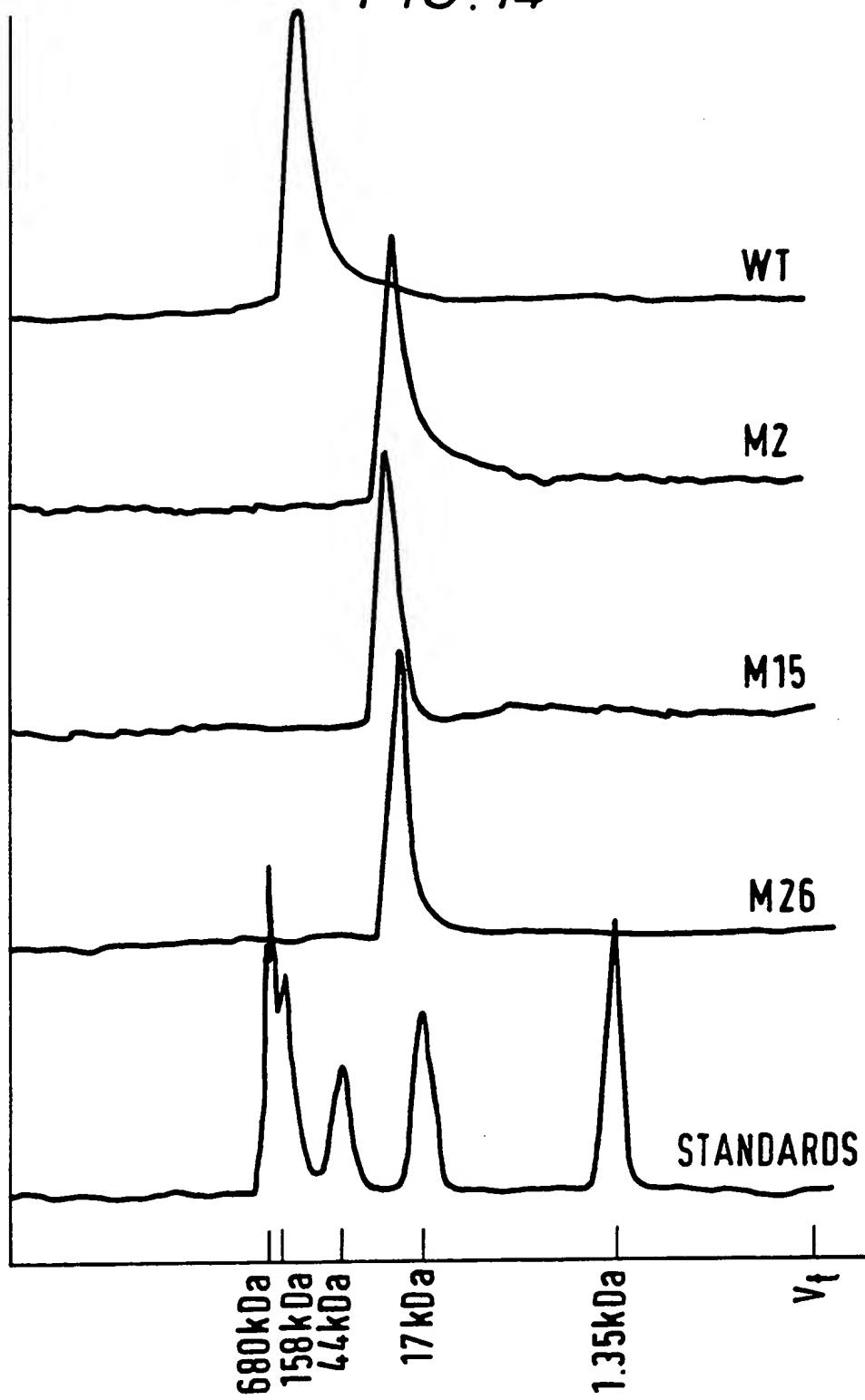


FIG.15A

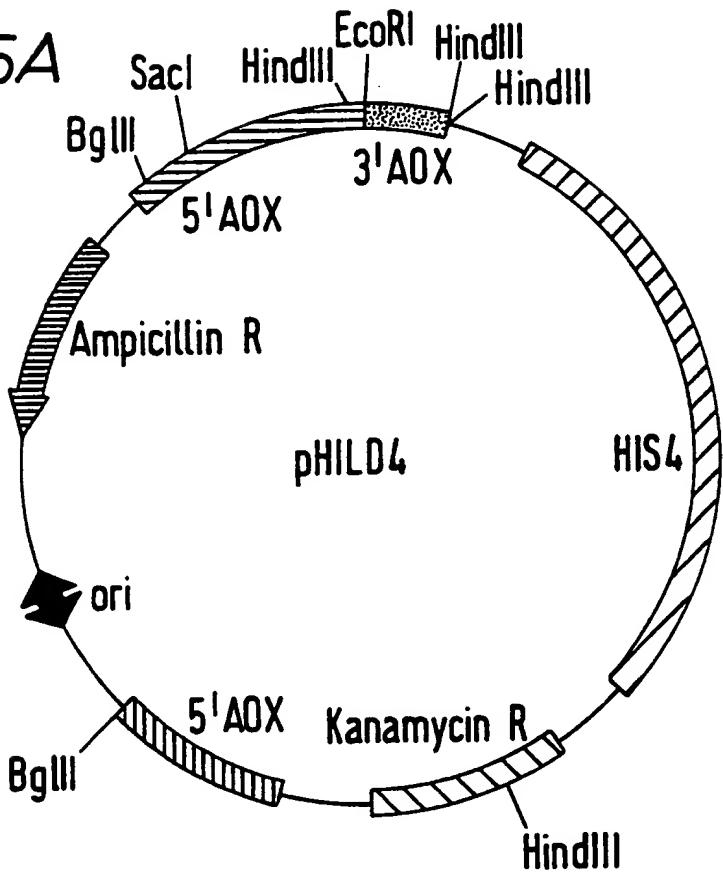


FIG.15B

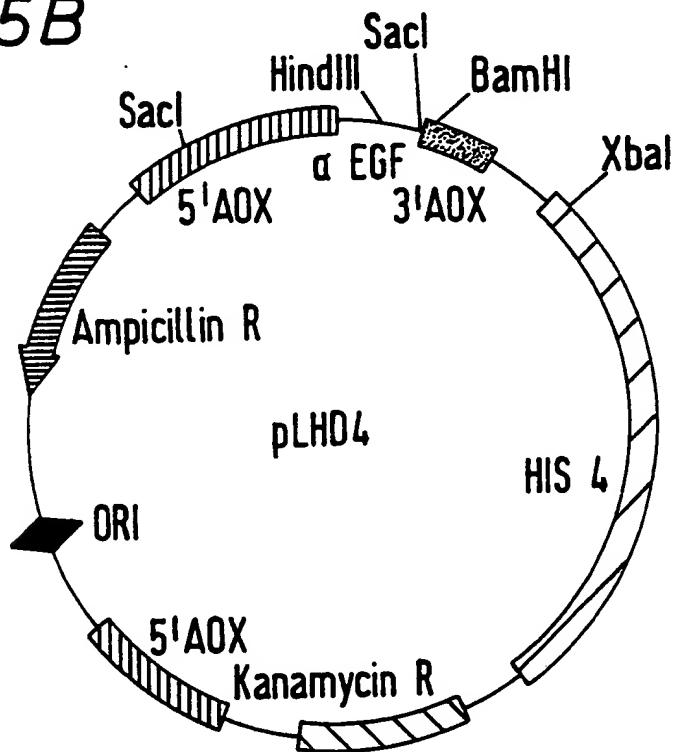


FIG. 16

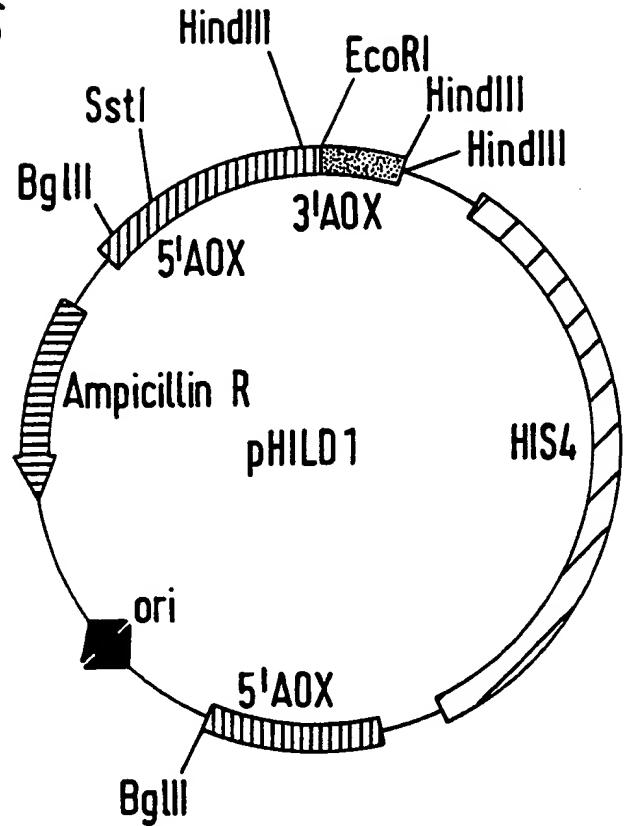


FIG. 17

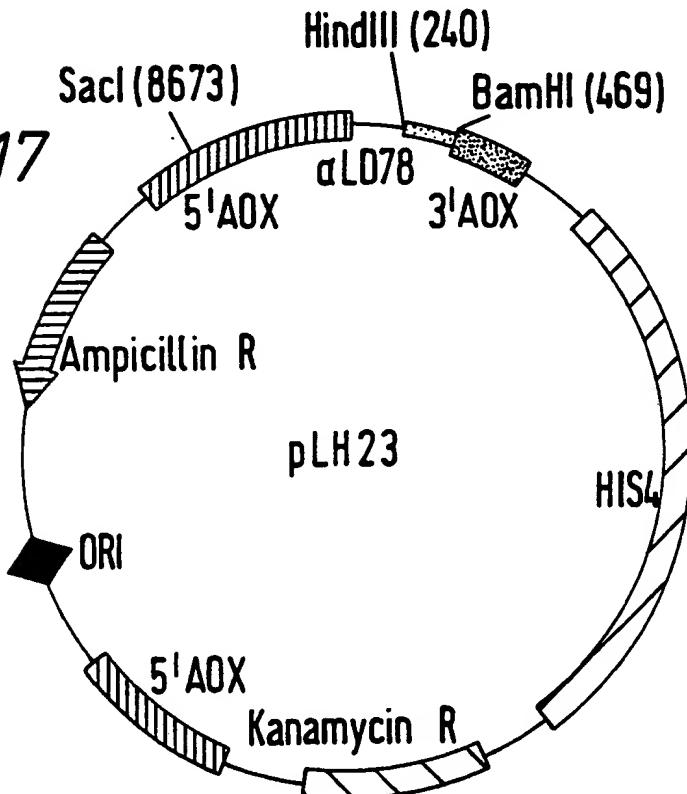


FIG. 18

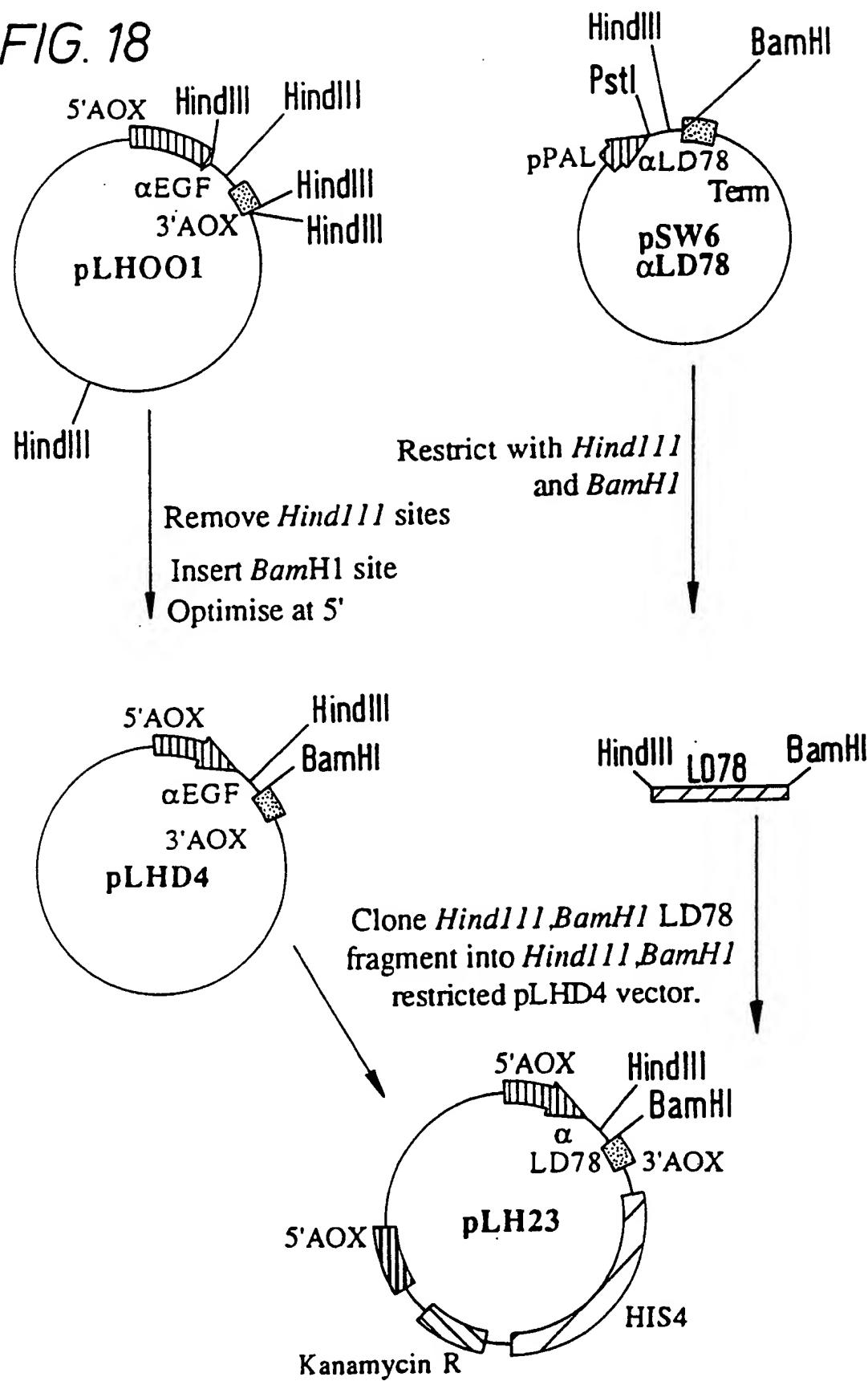
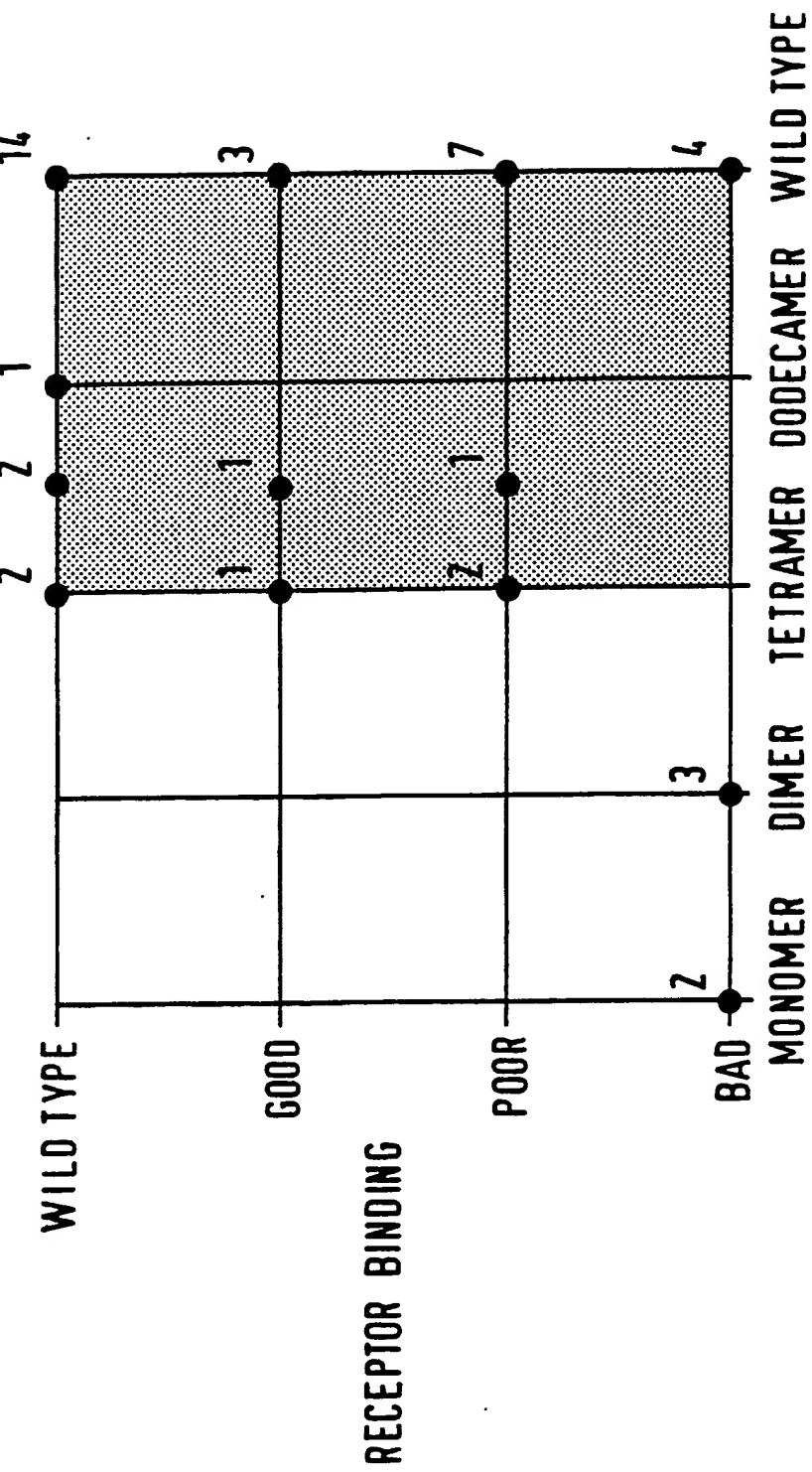


FIG. 19



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FIG. 20

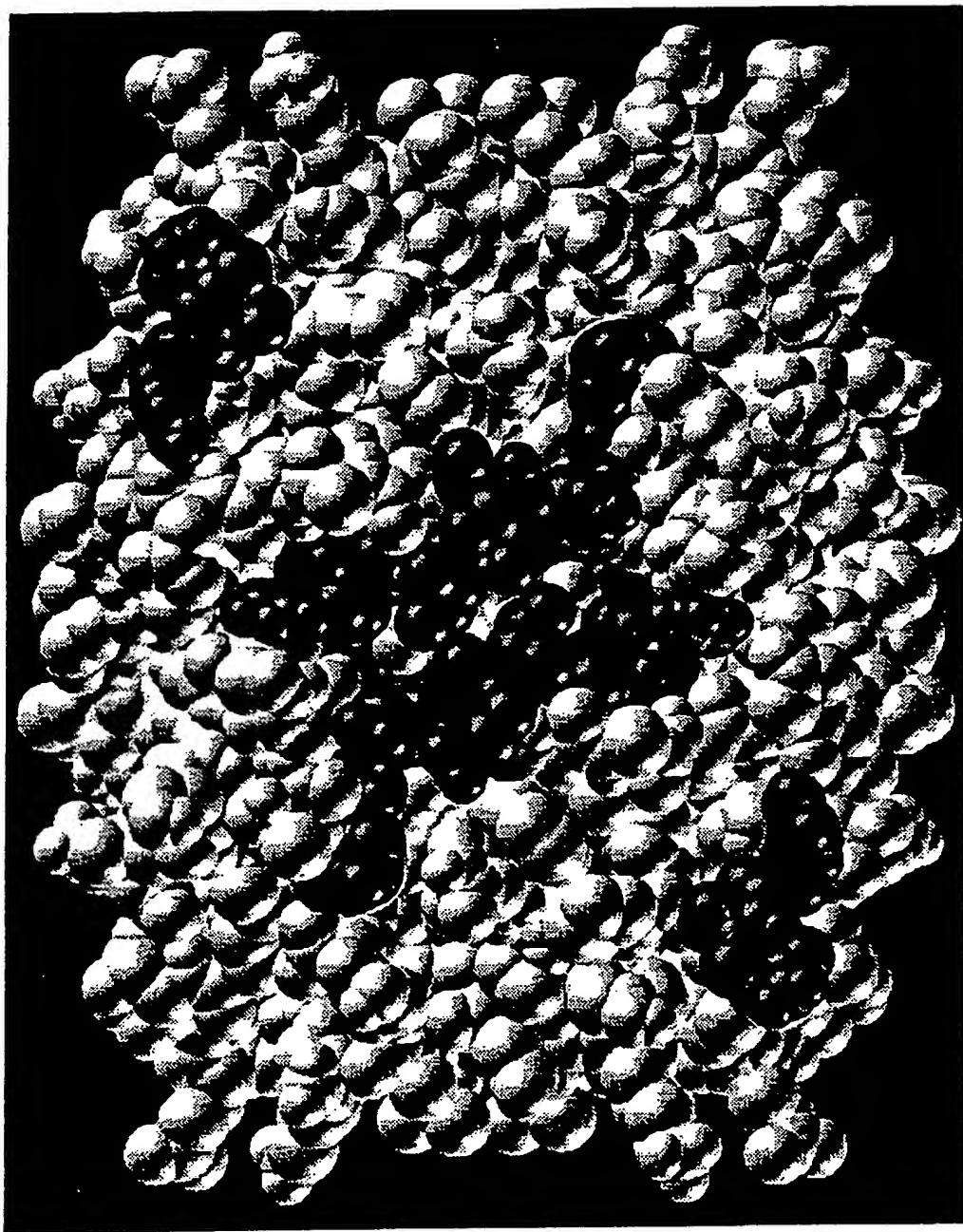


FIG. 21

AGCTTGGAT AAAAGATCCT TGGCTGCTGA CACTCCAACC GCTTGT TGTT TCTCTTACAC
 |||||
 ACCTA TTTCTAGGA ACCGACCGACT GTGAGGTTGG CGAACAAACAA AGA GAATGTG
 BB5615 BB5616

20 / 23
 CTCTAGACAA ATTCCACAAA ATTTCATTC TGACTA CTTT GAAACTCTT CTCAATGTTCTGA
 |||||
 GAGATCTGTT TAAGGTGTT TAAAGTAACG ACTGATGAAA CTT TGAAGAA GAGTACAAG
 BB5617 BB5618
 BB5619
 CAAGCCAGGT GTCATCTCT TGAC TAAGCC CTCGGAGACAA
 |||||
 GTTCCGGTCCA CAGTAGAAGA ACTGATTCCC G AGCTCTGTT CAGACACGAC TGGGTAGACT
 BB5620 BB5621
 BB5622

BB5623
 AGAAATGGTT CAAAATATG TTTCTGACTT GGAATTGTCT GCCTAATAAG
 |||||
 TCTTACCCAA GTTTTA TAC AAAGACTGAA CCTTAACAGA CGGATTTC CTAG
 BB5624

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FIG. 22

BB3374 AGCTTACCT GCCATGGCC CTTATGGAGC TGACACCC G ACTGCATGCT GCTTCTCCTA
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
ATGGA CGGTACCGCG GAATACTCG ACTGTGGGC TGACGT ACGA CGAAGAGGAT
BB3375

BB3376 CAGCCGAAG ATTCCACGCC AAT TCATCGT CGACTATTG GAAACTAGTA GCCTTTGCTC
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
GTCCGGCTTC TAAGGTGGGG TAAAGTAGCA GCTGATAAAA CTTTGATCAT CGGAAACCGAG
BB3377 BB3378
BB3379

BB3380 CC AGCCAGGT GTCATTTCC TGACTAAGAG AAACCGGA G ATCTGCCGCTG ACTCCAAGA
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
GGTCGGTCC A CAGTAAAGG ACTGATTCTC TTTGCCGTC TAGACC CGAC TGAGGTTCT
BB3381

BB3382 3B3382 GACCTGGTC CAAGAATAACA TCA CTGACCT CGACTGAAAT GCCTGATAGG ATCCG
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CTGGACCCAG GTTCTTATGT AGTGACTGGA GCTCCGACTTA CGGACTATCC TAGGCTTAA
BB3383 BB3385

FIG. 23

BB5424 AAAAGGAC CAATGGGTTCAAGACCCTCCA ACCGCAT GCT GCTTTTCTTA
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
ACCTA TTTTCTCGTG GTTACCCAAG TCTGGGAGGT TGGCGTACGA CGAA AAGAAT
BB5425

BB5426 AAGTTGCCATA GAAACTTTGT GGTC GACTAC TATGAGACCT BB5428
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CACCGCTAGG TTCAACGGAT CTTGAAACA CCAGCTGATG A TACTCTGGAA GAAGAAACAC
BB5427

BB5427 TCCAAACCAA AAGATCCAAG CAAGTCTGTG CTGACCCGAG
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CTCCCAGCCA GCTGTGGTAT CGACACCATA AGCTTTC GTT TTCTAGGTTTC GACTGGGCTC
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
GAGGGTGGT BB5429

BB5430 TCCAAACCAA AAGATCCAAG CAAGTCTGTG CTGACCCGAG
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CTTCAGCCA GCTGTGGTAT CGACACCATA AGCTTTC GTT TTCTAGGTTTC GACTGGGCTC
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
GACTGGGCTC BB5431

BB5432 TGG GTCCAGGAGT ACCTGTATGA CTTGGAATTG AACTGATAAG
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
TGAATCC ACTTAGGACC CAGG TGCACATACT GAACCTAAC TTGACTATTG CTAG
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
BB5433

FIG. 24

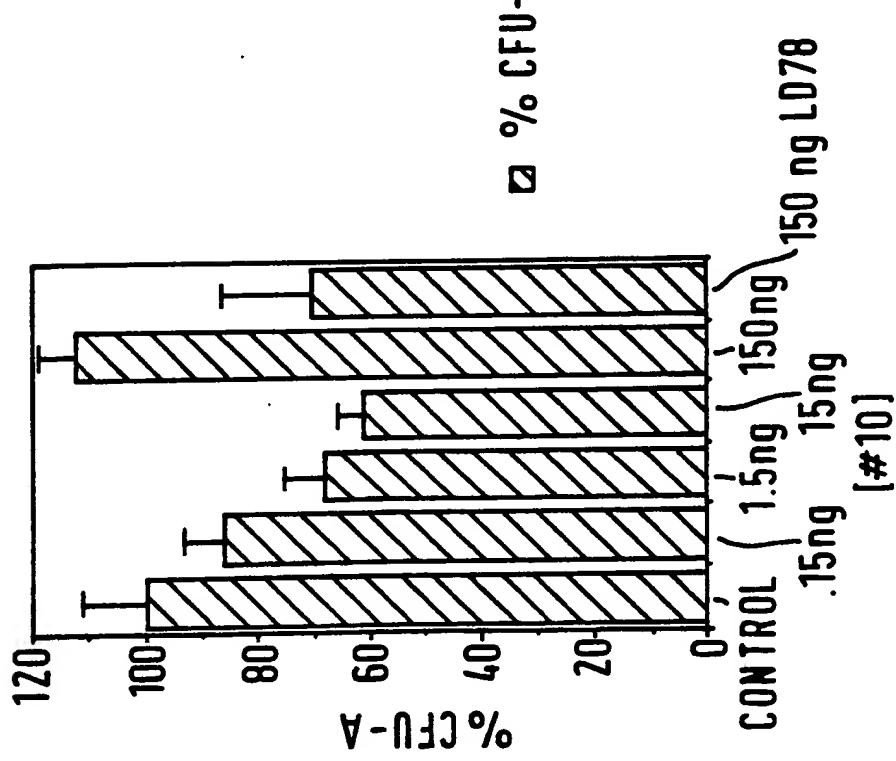
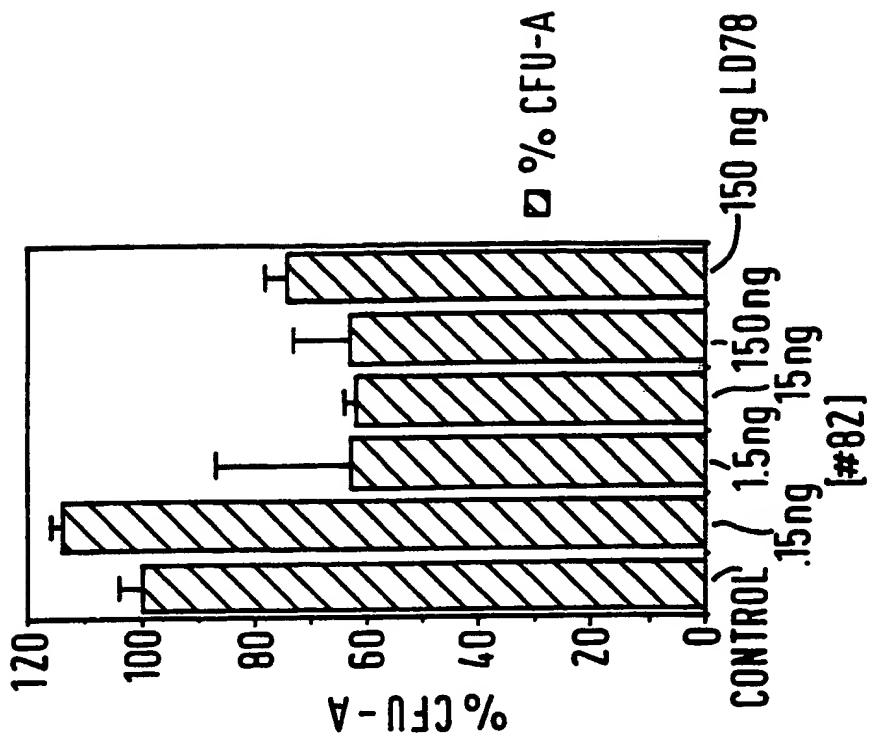


FIG. 25



I. CLASSIFICATION OF SUBJECT MATTER (If several classification symbols apply, indicate all)⁶

According to International Patent Classification (IPC) or to both National Classification and IPC

Int.C1. 5 C12N15/19;

C07K15/00;

C12N1/19;

A61K37/02

II. FIELDS SEARCHED

Minimum Documentation Searched⁷

Classification System	Classification Symbols			
Int.C1. 5	C07K ;	C12N ;	C12P ;	A61K

Documentation Searched other than Minimum Documentation
to the Extent that such Documents are Included in the Fields Searched⁸III. DOCUMENTS CONSIDERED TO BE RELEVANT⁹

Category ¹⁰	Citation of Document, ¹¹ with indication, where appropriate, of the relevant passages ¹²	Relevant to Claim No. ¹³
A	<p>MOLECULAR PHARMACOLOGY vol. 38, no. 3, September 1990, pages 401 - 409</p> <p>W.R.PAUKOVITS ET AL. 'Hemoregulatory peptide pGlu-Glu-Asp-Cys-Lys: A new synthetic derivative for avoiding dimerization and loss of inhibitory activity' see page 401, left column, paragraph 1 - page 402, left column, paragraph 3 see page 407, left column, last paragraph - page 408, right column, paragraph 2 ---</p>	1,2,4,5, 38,39
A	<p>WO,A,9 104 274 (GENETICS INSTITUTE, INC.) 4 April 1991</p> <p>see page 7, line 1 - line 10 see page 23, line 1 - line 15 see page 23, line 22 - page 26, line 7 ---</p>	1,29-34 -/-

¹⁰ Special categories of cited documents :¹⁰^{"A"} document defining the general state of the art which is not considered to be of particular relevance^{"E"} earlier document but published on or after the international filing date^{"L"} document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)^{"O"} document referring to an oral disclosure, use, exhibition or other means^{"P"} document published prior to the international filing date but later than the priority date claimed^{"T"} later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention^{"X"} document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step^{"Y"} document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.^{"Z"} document member of the same patent family

IV. CERTIFICATION

Date of the Actual Completion of the International Search 11 MARCH 1993	Date of Mailing of this International Search Report 24. 03. 93
International Searching Authority EUROPEAN PATENT OFFICE	Signature of Authorized Officer MONTERO LOPEZ B.

III. DOCUMENTS CONSIDERED TO BE RELEVANT

(CONTINUED FROM THE SECOND SHEET)

Category*	Citation of Document, with indication, where appropriate, of the relevant passages	Relevant to Claim No.
A	<p>Section Ch, Week 9147, Derwent Publications Ltd., London, GB; Class B04, AN 91-343166 & JP,A,3 228 683 ((KAGA) KAGAKU OYABI KESSEI) 9 October 1991 see abstract</p> <p style="text-align: center;">---</p>	23,24
P,X	<p>WO,A,9 205 198 (CHIRON CORPORATION) 2 April 1992 see page 6, paragraph 4 - page 7, paragraph 1 see page 13, paragraph 2 - page 15, paragraph 1</p> <p style="text-align: center;">-----</p>	37

**ANNEX TO THE INTERNATIONAL SEARCH REPORT
ON INTERNATIONAL PATENT APPLICATION NO.**

GB 9202390
SA 68542

This annex lists the patent family members relating to the patent documents cited in the above-mentioned international search report.
The members are as contained in the European Patent Office EDP file on
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Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO-A-9104274	04-04-91	CA-A- 2064558 EP-A- 0494268	26-03-91 15-07-92
WO-A-9205198	02-04-92	None	

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